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R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W. Bicchem Biophys. Res. Commun. 247, 367-372, 1998
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum albu A;Reference number: PD0018; MUID:98308123; PMID:9642133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agglutinin I precursor - European elder
C;Species: Sambucus nigra (European elder)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: 862627; 862619
R;van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Bur. J. Blochem. 235, 1128-137, 1996
A;Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A;Reference number: 862619; MUID:96202926; PMID:8631319
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A;Accession: S62619
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     ; Pred. No. 1.2e-19; 48; Mismatches 64
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A.Residues: 29-39;109-319 < VA2>

C.Superfamily: ricin; RNA N-glycosidase homology

F;37-283/Domain: FRNA N-glycosidase homology < RNG>
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A;Molecule type: mRNA
A;Residues: 1-570 <VAN>
Best Local Similarity
Matches 64; Conserv
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A, Accession: PD0018
A; Molecule type: protein
A; Mesidues: 1-254 cEGC-
C; Superfamily: ricin; rRNA N-glycosidase homology cRNG-
C; Superfamily: ricin; rRNA N-glycosidase homology
E; 7-246/Domain: rRNA N-glycosidase homology
C; Superfamily: rRNA N-glycosidase homology
Best Local Similarity 38.4%; Score 286; DB 2; Length 254;
Best Local Similarity 38.4%; Pred. No. 2.4e-18;
Best
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
1409.756 Million cell updates/sec February 10, 2004, 16:13:55; Search time 6.67161 Seconds Run on:

US-10-083-336A-10

1 MIFPKQYPIINFTTAGATVQ......RFQYIEGEMRTRIRYNRRSA 200 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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### ALIGNMENTS

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RICI_RICCO STANDARD; PRT; 576 AA.
P02879; P02880;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2013 (Rel. 42, Last annotation update)
16-SEP-2013 (Rel. 42, Last annotation update)
18-SEP-2021; Ricin B chainly.
Ricinus communis (Castor bean).
Ricinus communis (Castor bean).
Ricinus (Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tregear J.W., Roberts L.M.;
"The lectin gene family of Ricinus communis: cloning of a functional
"ricin gene and three lectin pseudogenes.";
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MEDLINE-86067214; PubMed-2999712;
Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE OF 12-576 FROM N.A.
MEDLINE-85179479; Pubmed-3838723;
Lamb A., Roberts L.M., Lord J.M.;
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"Isolation and sequences of peptic peptides, and the complete sequence of Ile chain of ricin-D.";
Agric. Biol. Chem. 42:1267-1274(1978).
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Funateu G., Kimura M., Funatsu M.;
"Primary structure of Ala chain of ricin D.";
Agric. Biol. Chem. 43:2221-2224(1979).
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SIMILARITY: Contains 2 ricin B-type lectin domains.
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Kin Y., Robertus J.D.;

Analysis of several key active site residues of ricin A chain by

"Analysis of several key active site residues of ricin A chain by

"Thangenesis and X-ray crystallography.";

The with site of several key active site residues of ricin A chain by

The with site of several key active site residues of ricin A chain by

The cream S.775-779(1992).

The rotein Brown S.775-779(1992).

The rotein synthesis through the catalytic inactivation of 60S protein specific adenine residue from an exposed loop of 28S ribosomal subvolved in the binding of elongation factorist the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can herefore kill an animal cell againtination (Lectin activity). It binds to beta-D-

The coll again of the A chain, and cativity). It binds to beta-D-

The coll again of the cell again and cativity). It binds to beta-D-
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-! SUBUNIT: Disulfide-linked dimer of A and B chains.
-! DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologus subdomains (alpha, beta, gamma).
-! PIM: THE MANOR A-CHAIN IS GIYCOSYLATED DONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GIYCOSYLATED ALSO IN POSITION 271.
-! SIMILARITY: IN THE N-TERRINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."; J. Mol. Biol. 244:410-422(1994).
                                                                  MEDLINE=87165983; PubMed=358397;
Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B.,
Rutember E., Xuong N.H., Hamlin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
J. Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96374222; PubMed=8780513; Day P.J., Enrst S.R., Frankel A.E., Monzingo A.F., Pascal J.M., Molina-Svinth M.C., Robertus J.D.; Molina-Svinth M.C., Robertus J.D.; "Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97240820; PubMed-9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J., Pauptit R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=91352005; PubMed=1881882;
Rutember E., Robertus J.D.;
"Structure of ricin B-chain at 2.5-A resolution.";
Proteins 10:260-269(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
                                                                                                                                                                                                                    MEDLINE-91352004; Pubmed-1881881; Katzin B.U., Collins E.U., Robertus J.D.; "Structure of ricin A-chain at 2.5 A."; Proteins 10:251-259(1991).
                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 35:11098-11103(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95082010; PubMed=7990130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactopyranoside moieties.
                           Toxicon 39:1723-1728(2001).
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 CONFLICTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO03-6; SHIGARICIN.
SMART; SMO458; RIGIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
PLANT defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FIId=CAR 000080.
N-LINKED GLCNAC. .) (IN MINOR FORM).
/FIId=CAR 000081.
N-LINKED GLCNAC. .).
E -> D (IN REF. 3).
A -> R (IN REF. 3).
-!- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFL. WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3)
-!- DATABASE: NAME=Protein Spotlight;
                                                        NOTE-Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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2-BETA.
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1-GAMMA.
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InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                     EMBL; X03179; CAA26939.1; -.
EMBL; X52908; CAA37095.1; -.
EMBL; X02388; CAA26230.1; -.
EMBL; A12892; CAA01058.1; -.
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14-JAN-98.
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11L9; 16-JAN-02
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Best Local Similarity 92.0
Matches 183; Conservative
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466
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564 AA;
PIR; A24261; RLCSAG.
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P28590;
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DISULFID
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DOMAIN
BOMAIN
REPEAT
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REPEAT
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ABRC ABRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                121
                                                                                                                                        ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                  181
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                                                              61
                                                                                      95
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                                                                                     36 IFPKQYPIINETTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFG
                                                                                                                                                                 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Malpighiales, Euphorbiaceae, Ricinus.
                                                              2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Araki T., Yoshioka Y., Funatsu G.; The Complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285(1986).
                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-Bylcosidase) (EC 3.2.2.2); Agglutinin B chain].
                                      ö
              Length 576;
                                      Indels
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              Score 1024; DB 1;
Pred. No. 1.1e-87;
  99.5%; Scort No. 1...
V 100.0%; Pred. No. 1...
O; Mismatches
                                                                                                                                                                                                                                                                                                           564 AA
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                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                          216 FOYIEGEMRTRIRYNRRSA 234
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01-JAN-1988 (Rel. 06, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                    (Castor bean)
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                                        Matches 199; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE OF 303-564.
                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3988;
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P06750;
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                                                                                                                                          96
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             Query Match
Rest Local ;
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RESULT 2

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62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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                                      Pfam; PF00652; Ricin B_lectin; 6.
Pfam; PF00652; Ricin B_lectin; 6.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00396; SHIGARICIN.
PROSITE; PS00215; SHIGA B_LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
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INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..).

N-LINKED (GLCNAC. ..).

N-LINKED (GLCNAC. ..).

F -> T (IN REF. 2).

N -> D (IN REF. 2).

R -> T (IN REF. 2).
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor (Contains: Abrin-c A chain (rRNA N-glycosidase)
(BC 3.2.2.22); Abrin-C B chain).
Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                         AGGLUTININ B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                       AGGLUTININ A CHAIN.
LINKER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.8%; Score 934.5; DB 1
92.0%; Pred. No. 2.3e-79;
iive 7; Mismatches 8
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2-ALPHA.
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HSSP; PO2879; 1BR6.
GIYCOSUILEDB; PO6750; -
InnerPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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LEUT. J. BIOCHEM. 198:723-732(1991).

- I. FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN THE CATALYTIC INACTIVATION OF 60S RIBOSONAL SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSONAL SUBDINITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE CHAIN IS A GALACTOSE-SPECIFIC IECTIN THAT FACLLITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

- !- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

- !- SUBBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS, BELING, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstands the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RĪCIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                   MEDLINE=91266957; PubMed=2050149;
Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;
"Preproabrin: genomic cloning, characterisation and the expression of
"he A-chain in Escherichia coli.";
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
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INTERCHAIN (BY SIMILARITY).
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1-BETA.
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2-ALPHA.
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InterPro; IPR001574; RIP.
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SIGNAL 1 34
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435
562 AA;
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                                                                                      SEQUENCE FROM N.A.
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                                                     NCBI_TaxID=3816;
                                                                                                       TISSUE=Leaf
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DB 1; Length 562;

34.4%; Score 353.5;

Query Match

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93 SERESIEVGIDVTNAXVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                                                                                                                                                                                                  126 RIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                            149 DIERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI 205
                                                                                                                                                        66 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rBNA.
-!- SUBMIT: DISULFIDE-LINEED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: CONTAINS 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 3.2.2.21); ADTIN-D B CRAIN].
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                         6 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                   9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Seed;
MEDLINE=93169023; PubMed=7763422;
Kimura M., Sumizawa T., Funatsu G.;
Kimura M., Sumizawa T., Funatsu G.;
Kimura M., Sumizawa T., Funatsu G.;
The complete amino acid sequences of the B-chains of abrin-a and
abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biosci. Biotechnol. Biochem 57:166:169 (1993).
-!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENING FROM POSITION 4,324 OF 28 S. RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABRB ABRRR STANDARD; PRT; 527 AA.

10.0077; PB1374;
15.DEC-1998 (Rel. 37, Created)
15.DEC-1998 (Rel. 37, Last sequence update)
15.DEC-1998 (Rel. 37, Last sequence update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(EC 3.2.2.2); Abrin-b B chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                   70; Indels
45.5%; Pred. No. 2.6e-25;
tive 24; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93132798; PubMed=8421313;
                          Conservative
                                                                                                                                                                                                                                                                                                                                                   186 EGEMRTRIR 194
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Best Local Similarity
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PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
CHAIN 150 LABRIN-B A CHAIN.
PRPTIDE 251 260 LINKER PEPTIDE.
CHAIN 272 ABRIN-B CHAIN.
DOMAIN 272 ABRIN-B TOXIN B-TYPE LECTIN 1.
DOMAIN 402 526 RICIN B-TYPE LECTIN 2.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.5%; Score 345; DB 1; Length 527
45.5%; Pred. No. 1.5e-24;
ive 22; Mismatches 72; Indels
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BY SIMILARITY
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H -> T (IN REF. 2).
i. 3253AE490CE9494A CRC64;
rength
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D -> N (IN REF. 2).
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EMBL; M98345; AAA32625.1; -.
PIR; S32430; S32430.
HSSP; P11140; 1ABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                            Pfam; PF00652; Ricin B_lectin; 6. Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN. SMARY; SM00458; RICIN; 2.
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RESULT

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-!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT INACTIVATES EUKRARYOTIC GOS RIBOSOMAL SUBUNITS.
-!- CATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-!- TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chow T., Feldman R.A., Lovett M., Platak M.,
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                                                                                                                           Bukaryota, Viridiplantae, Střeptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
application.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 24-270.
STRAIN=Maximowicz; TISSUE=Tuberous root;
MEDLINE=90256789; PubMed=2341399;
COllins B.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R., Wu P., Hwang K., Piatak M.;
"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                           STRAIN=Maximowicz;
MEDIJINE=9115367; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=95344383; PubMed=7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298 (1995).
                                                         01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SIP-2003 (Rel. 42, Last annotation update)
15-SIP-2003 (Rel. 42, Last annotation update)
17-SIP-2003 (Rel. 42, Last annotation precursor (RRNA N-glycosidase) (RC.3.2.2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=94344957; PubMed=8066085;
Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
289 AA
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Maximowicz, TISSUB=Leaf;
MEDLINE=90256790; PubMed=2341400;
                                       01-MAR-1989 (Rel. 10, Created)
    STANDARD;
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              EMEL; M34858; AAA34207.1; -.

DR EMEL; M34858; AAA34206.1; -.

DR PIR; JT0566; RLTZT.

DR PDB; INCA; 07-FEB-95.

DR PDB; ILGS; 10-JUL-95.

DR PDB; ILGS; 28-JAN-03.

R PDB; ILGS; 28-JAN-03.

R PDB; ILGS; 28-ARR-00.

R PCSTTE; PRO01574; RIP.

R PROSITE; PRO0275; SHIGARICIN.

R PROSITE; PR
                                                                                                                                                                                                                                       | DEL -> LELI (IN REF. 4).
| MISSING (IN REF. 4).
| I -> L (IN REF. 4).
| V -> VDACLPENAVL (IN REF. 4).
| KI -> GL (IN REF. 4).
| KI -> GL (IN REF. 4).
| K -> S (IN REF. 4).
| WS -> LWL (IN REF. 4).
| WS -> IWL (IN REF. 4).
| WS -> IWL (IN REF. 5).
| WS -> IWL (IN REF. 5).
| MISSING (IN REF. 2).
| MISSING (IN REF. 2).
| T -> M (IN REF. 2).
                                                                                                                                                                                                         TRICHOSANTHIN.
MISSING IN MATURE PROTEIN.
BY SIMILARITY.
   or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates.";

Bioconj. Chem. 5:423-429(1994).

-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

-!- CARALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-!- SIMILARITY: BLOOMS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIPE BRYDI STANDARD; PRT; 282 AA.
P99184; QS810;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
glycosidase) (EC 3.2.2.2) (BD2).
Bryonia dioica (Red bryony).
Bryonia dioica (Red bryony).
Sparmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                          25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                 70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Siegall C.B., Gawlak S.L., Marquardt H.;
"Bryodin 2 a ribosome-inactivating protein isolated from the plant
                                                                                                                                                     Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Root;
BEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff B.A., Mixan B.,
Marquardt H.;
                                                                                       31676 MW; 5CE09BB630575BB9 CRC64;
                                                                                                                                                 33.2%; Score 342; DB 1; Similarity 39.5%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent number US5597569, 28-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 134238; -; NOT_ANNOTATED_CDS.
HSSP; P09989; 1MRJ.
                                                                                                                                        Query Match
Best Local Similarity 39.5%;
260 2
263 2
266 2
289 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bryonia dioica.
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                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                           69 LSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVONRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                               81 BSVTVALDVVNVYVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLE 136
                                                                                                                                                                                                                                                                                                10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPN-RVGLPINQRFILVELSNHAE 68
                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 QLAGNI-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem. Pharm. Bull. 39:1244-1249(1991).

-!- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
60S RIBOSOMAL SUBUNITS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizukami H., Iida K., Kondo T., Ogihara Y.; "Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes kirilowii var. japonica.";
                                                                                                                                                                                                                                                                                                                                    24 INFSLIGATGATYKTFIRNLRTKÍTVGTPRVYDÍÞVÍRNAAAGÍ---ARFQÍVTLTNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Střeptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                            RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                              -LINKED (GLCNAC. . .) (POTENTIAL). C52BE2F6A873769C CRC64;
                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92005921; PubMed=1914000;
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,
                                                                                                                                                                                                                     Score 341.5; DB 1; Length 282; Pred, No. 1.5e-24; 3; Mismatches 57; Indels 13
                   Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGALCIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.22).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                  BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AA
                                                                                                                                                                                                                                                               23; Mismatches
                                                                                          Multigene family; Glycoprotein; Signal. SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kirilowii var. japonica.";
Biol. Pharm. Bull. 20:711-713(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=97356562; PubMed=9212998;
                                                                                                                                                                                     282 AA; 30754 MW;
                                                                                                                                                                                                                             33.2%;
                                                                                                                                                                                                                                           48.0%;
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InterPro; IPR001574; RIP.
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183
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183
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P24478:
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                 82 IISVAIDVINVYVMGYRAGDISYFF---NEASAIEAAKYVFKDAKRKVILPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 QLAGNIRENIELGNGPLEEAISALXYXSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                      10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=56215449; PubMed=8647092;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
fingerin b), a GallAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 22:1181-1186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p33183; P33184; P93542;
01-0CT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-91ycosidase) (EC 3.2.2.2; Nigrin b B chain).
                                                                                                                                                                                                                                                                                                       12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                          PIR; JC5606; JC5606.

PIR; JU0393; JU0393.

HSSP; P09989; LIMJ.

InterPro; IPR001574; RIP.

Pfam; PF00161; RIP; 1.

PRNTS; P800396; SHIGARICIN.

PROSITE; P800275; SHIGARICIN; 1.

PROSITE; P800275; HGAR RICIN; 1.

Plant defense; AntiviraT; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                          Length 289;
                                                                                                                                                                                                                                                                                                       53; Indels
                                                                                                                                                                                                                                           883D3E3242887B26 CRC64;
                                                                                                                                                                                                            REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                            32.8%; Score 338; DB 1; 40.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AA.
                                                                                                                                                                                                                                                                                                           46; Mismatches
                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                               KARASURIN-C.
KARASURIN-A.
                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=94003077; PubMed=8400135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sambucus nigra (European elder).
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                                                                                                                                                                                                                                             289 AA; 31704 MW;
           EMBL; AB000666; BAA21786.1;
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                  21
270
270
289
183
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                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                       roxin; Signal
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SEQUENCE
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142 DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Lin J.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.
"The complete primary structure of abrin-a B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Biol. Chem. 266:6848-6852(1991).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91201329; PubMed=2016300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-251 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECEDES ENDOCYTOSIS.
                                                                                                                                                            STANDARD;
                                      185 IEGEMRTRIR 194
                                                          || |:| ::
195 IEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 262-528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-251.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3816;
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                                                                                                                                                            ABRA ABRPR
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                                                                                                                                             ABRA_ABRPR
                                                                                                                           RESULT 9
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI --THLFTDVQNRYTFAFGGNY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVOKSNLFVGTKON-TLSFTGNY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 YPSVSFNIDGAKSATYRDFISNIRKTVATGTYEVNGLÞVIRRESEVQVKSRFVLVPLTNY 87
     PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 STRNA. THE B-CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                                                               one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS50231; RICINBLECTIN; 2.
PROSITE; PS50231; RICINBLECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
SIGNAL
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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Matches 75, Conservative
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Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic
"The complete amino acid Rabrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
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-!- SUBUNIT: DISULFIDE-LINKED DIMEN OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERNIAL, SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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01-JUL-1989 (Rel. 11, Created)
01-JUN-1984 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
(RC 3.2.2.2); Abrin-a B chain!
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993)
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70 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 127
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N-LINKED (GLCNAC. . .).
N-SINKE (IN REF. 4).
N -> Y (IN REF. 4).
N -> Y (IN REF. 4).
T -> P (IN REF. 4).
V -> L (IN REF. 4).
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28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
RC 3.2.2.22) (BD1).
Bryonia dioica (Red bryony).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica.";
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SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE I RIP SUBFAMILY.
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Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.
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Int. J. Pept. Protein Res. 33:263-267(1989).
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Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.
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01-007-1993 (Rel. 27, Created)
16-007-2001 (Rel. 40, Last sed)
28-FEB-2003 (Rel. 41, Last ann
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                 EMBL, 124020; -; NOT ANNOTATED_CDS.
PIR, S16491; S16491.
PDB; LBRY, 0.4-MAR-98.
InterPro; IPRO01574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN, 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; 3D-structure; Multigene family; Glycoprotein; Signal.
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Best Local Similarity 37.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                              129 ÖLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                          10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLIPSASGA---SRYILMQLSNYDAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Islam M.R., Hirayama H., Funatsu G.;
"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-238(1991).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
S SFRISGATITSYGVEIKNLREALPYERKV-YNIPLL--RSSISGSGRYTLLHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 3.2.2.2).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AVG-1991 (Rel. 19, Created)
01-AVG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
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                                                                                                                                                                                                                                                                                                                                                                                                                            250 AA.
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91248488; PubMed=136866;
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                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JN0108; JN0108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                             189 MRTRI 193
                                                                                                                                                                                                                                                                                                            194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=seed;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 NIITMAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Yamada T., Ohki S.T., Osaki T.;

"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";

Plant Biotechnol. 17:337-340(2000).

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL-PNRVGLPINQRFILVELSNHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 VKFSLLGSNHKSYSKEITSMRNALPNAGDI-YNIPLLVPSISG---SRRYILMQLSNYBG
                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1; Cucurbitales, Cucurbitaceae, Cucumis.
NCBI_TaxID=131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%; Score 296.5; DB 1; Length 286;
llarity 34.4%; Pred. No. 2.3e-20;
Conservative 47; Mismatches 64; Indels 13; Gaps
                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001574; RIP.
PERNTS; PR00151; RIP, 1.
PRINTS; PR00396; SHIGARICIN.
PROSTTE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 21 POTENTIAL.
12 286 PUTATIVE RIBOSOME-INACTIVATING PROTE 185 186 BY SIMILARITY.
103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
286 AA; 31771 MW, 4EFD4966E604DA41 CRC64;
286 AA
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HSSP; P16094; 1AHC.
STANDARD;
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ses 65; Conserv
                                                                                                                                                                                                                Cucumis figarei
CUCFI
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CARBOHYD
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RIP1 CU
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S.

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PEBS Lett. 399:153-157(1996).

-! FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL

SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRAM. THE

B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY

INTO THE CELL OF THE A CHAIN! B CHAIN'S ARE ALSO RESPONSIBLE FOR

CELL AGGLUTINATION (LECTIN ACTIVITY).

-! ATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one

specific adenosine on the 28S TRNA.

-! SUBUNIT: Disulfide-linked dimer of A and B chains.
                                                                                                                                                                                                                                                                                                           "Complete amino acid sequence of the A chain of mistletoe lectin I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA'.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 2 RIP SUBFAMILY.
                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
18-PER-2003 (Rel. 41, Last annotation update)
18-ERB-2003 (Rel. 41, Last annotation update)
18-ERB-2003 (Rel. 41, Last annotation update)
18-ERB-2003 (Rel. 41, Last annotation update)
19-ERB-2003 (ML-I A) (rRNA N-Glycosidase) (EG 3.2.2.2.2).
Viscum album (European mistletoe).
                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Lectin.
                                                                                                                                                                                                                         SEQUENCE.
STRAIN=Subsp. album;
MEDLINE=97134581; PubMed=8980141;
SOler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%; Score 286; DB 1; Length 254; 38.4%; Pred. No. 1.9e-19; Live 36; Mismatches 56; Indels
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D -> S (IN MLA').
53BAF98D3E0FFE67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Toxin; Repeat; Glycoprotei:
5 165 BY SIMILARITY.
2 112 N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQ -> EE (IN MIA').
DQ -> BE (IN MIA').
T -> S (IN MIA').
T -> A (IN MIA').
T -> A (IN MIA').
Y -> D (IN MIA').
A -> E (IN MIA').
A -> E (IN MIA').
I -> F (IN MIA').
I -> F (IN MIA').
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V -> I (IN MLA')
254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.
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PRT;
                                                                                                                                                                Santalales; Santalaceae; Viscum.
NCBI_TaxID=3972;
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STANDARD;
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254 AA;
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ACT_SITE 169
CARBOHYD 113
                                                                                                                                                                                                                                                                                                Voelter W.;
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SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
67 TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                     132 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF-----Q 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VRFSLSGSSSTSYSKFIGDLRKALPSNGTVYNITLLLSSASGA---SRYTLMTLSNYDGK
                                                                                                                                                                                                                                                                                                                                                                   N-Gyrosiusae, inc. 22.1. Lofah) (Sponge gourd).
Luffa cylindrica (Smooth Loofah) (Sponge gourd).
Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Oucurbitales; Cucurbitaceae; Luffa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.; "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica."; Plant Mol. Biol. 18:1199-1202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 284.5; DB 1; Length 277; Pred. No. 2.9e-19;
                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
08-EPB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :69
                                                                                                                         -GEMRTRIRYN 196
                                                                                                                                                        179 YINSGASFLPDVYMLELETSWGQOSTQVQHS 209
                                                                                                                                                                                                                                                  277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Mismatches
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PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92288316; PubMed=1600156;
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277 AA; 30212 MW;
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InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3670;
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10;

56; Indels 38; Gaps

Conservative

81;

Similarity

72 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 131

9 THOTTGEEYPRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELINQGQDSV 14 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTOMISEAARFQYIEGEM 189
                                   InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSTIE; PS00275; SHIGA RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momordin II precursor (rRNA
N-glycosidase) (EC 3.2.2.22).
Momordica balsamina (Bitter gourd) (Balsam pear).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae,
NCBI_TaxID=3672;
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                                                                                                                                                                                                                                                                                                                                              286 AA.
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                              PRT;
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286
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PDB; 1CF5; 07-JUN-99.
                                                                                                                                                                                     191 IERISKNO 198
                                                                                                                           190 RTRIRYNR 197
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SEQUENCE FROM N.A.
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SIGNAL
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:17:00; Search time 26.6864 Seconds (without alignments) 1933.961 Million cell updates/sec Run on:

US-10-083-336A-10 Title:

1029 1 MIFPKQYPIINFTTAGATVQ.....RFQYIEGEMRTRIRYNRRSA 200 Perfect score:

Scoring table: Sequence:

830525 segs, 258052604 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: Sp\_archea:\*
2: Sp\_bacteria:\*
3: Sp\_fung1:\*
4: Sp\_fung1:\*
5: Sp\_invertebrate:\*
5: Sp\_invertebrate:\*
5: Sp\_mammal:\*
5: Sp\_mhc:\*
5: Sp\_mhc:\*
5: Sp\_mhc:\*
6: Sp\_mhc:\* sp\_virus:\*
sp\_vertebrate:\* rodent:\* sp\_plant:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp\_archeap:\*

sp\_unclassified:\*

sp\_bacteriap:\*

	SUMMAKLES	Description	1	294BW3 cinnamomum	Q94BW4 cinnamomum	294BW5 cinnamomum	Q9FV22 cinnamomum	1367 004367 sambucus ni	AVR2 Q9avr2 sambucus eb		Q94ke4	GP1re3 trichosanth	Q41216 Q41216 trichosanth		15S2 Q945B2 Bambucus ni	ST32 Q8gt32 sambucus ni	
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Len		Score	1021	401.5	397.5	397.5	395.5	350.5	347.5	344.5	340	338	338	336.5	330.5	330.5	
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323.5 323.5 314.5 314.5 314.5 314.5 314.5 282 282 282 282 282 282 282 282 282 28
7118900000000000000000000000000000000000

### ALIGNMENTS

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MEDINE-PROM N.A.

MEDINE-92338377; PubMed=1633111;

MEDINE-92338377; PubMed=1633111;

Molecular cloning of richn.;

Targeted Diagn. Ther. 7:81-97(1992).

"Molecular cloning of richn.";

Targeted Diagn. Ther. 7:81-97(1992).

"CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADBROSINE ON THE ZBS RRMA.

SPECIFIC ADBROSINE OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL: $40366; AAB22582.1; -..

RESP: PRO1979; IBR6.

RICHEPPO: IPR00172; Richn. B. lectin.

InterPro: IPR001400; Somatotropin.

REPRO: PF00161; RIP: 1...

PERM: PF00161; RIP: 1...

PERM: PF00161; RIP: 1...
                                                                                                                                                                                                                                                                                                                                                     Ricinus communis (Castor bean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;
                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
prorifoin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                             541 AA.
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SMART; SMO0458, RICIN, 2.
PROSITE, PS50231, RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN, 1.
PROSITE; PS00338; SOMATÖTROPIN_2; 1.
                                                                             PRT;
                                                                             PRELIMINARY;
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SEQUENCE 541 AA
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Q41174;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                               91
                                                                                                 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                               2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61
                                                                        1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTY: ENDOHYNDGLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AN0380913, ARK8A460.1; -.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECTION N.A. Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                              Cinnamomum camphora (Cāmphor tree).
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
NCBI_TaxID=13429,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.0%; Score 401.5; DB 10; Length 580; 50.0%; Pred. No. 3e-29; Live 28; Mismatches 59; Indels 7;
                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
17ppe 2 ribosome-inactivating protein cinnamomin III precursor (EC 3.2.2.2) (rRNA N-glycosidase).
  DB 10; Length 541;
                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          940D10F01E7FB558 CRC64;
99.2%; Score 1021; DB 10
99.5%; Pred. No. 9.3e-88;
ive 1; Mismatches 0
                                                                                                                                                                                                                                                                                           580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CINNAMOMIN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                     182 FQYIEGEMRTRIRYNRRSA 200
                                                                                                                                                                                                                      580 AA; 64421 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.0%
Best Local Similarity 50.0%
Matches 94; Conservative
                          Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
                          198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patterns."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                  62
   Query Match
Best Local &
                                                                                                                                                                                                                                                                                            Q94BW3
                          Matches
                                                                                                                                                                                                                                                                   RESULT 2
Q94BW3
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66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ON SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AV039802; ARK2459.1; -
InterPro; IPR000772; Richin_B_lectin.
                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II precursor
(EC 3.2.2.2) (rRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Cinnamomum camphora (Camphor tree).
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
TYPE 2 RIBOSOME-INACTIVATING PROTEIN
CINNAMOMIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y.; Yang O., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating progenes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.6%; Score 397.5; DB 10; Length 580; 49.5%; Pred. No. 7.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2001 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.2) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37E4289ECCEOCBFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 580 AA; 64265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 EGEMRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 EYRVRESI 214
186 EGEMRTRI 193
                                           207 EYRVRESI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patterns.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q94BW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                          094BW4
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InterPro; IPR000772; Ricin_B_lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AADSPVTLAVDVINAYVVAYRIGSQSFFLREDNPD--PAIENLIPDIK-RYTFPFSGSYT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 DLEGVAGERREEILLIGMDPLENAISALWISNL--NQORALARSLIVVIQMVAEAVRFRFI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xie L., Liu W.-Y., Wang E.-D.;
"Molecular cloning of cinnamomin A-, B-chain and the expression,
"Molecular cloning of cinnamomin A-, B-chain and the A-Chain.";
purification, characterization and mutagenesis of the A-Chain.";
submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
HSSP; P02879; 2AAI.
                                                                                                                                      Submitted (UTN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLXSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADBROSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039801; AAK82458.1; -..
InterPro; IPR000772; Ricin.B.lectin.
InterPro; IPR001574; Ricin.B.lectin.
Pfam; PF00662; Ricin.B.lectin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Yang Q., Gong Z.Z., Liu W.Y.,

"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 YPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (BC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
              Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales; Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                          TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN I.
                                                                                                                                                                                                                                                                                                                                                                                              38.6%; Score 397.5; DB 10; Length 581; 50.0%; Pred. No. 7.1e-29; tive 27; Mismatches 60; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                      GEBF5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                     SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cinnamomum camphora (Camphor tree)
Eukaryota; Viridiplantae; Streptopl
    Cinnamomum camphora (Camphor tree)
                                                                                                                                                                                                                                                                                                                                                                        581 AA; 64215 MW;
                                                                                                                                                                                                                                                                         PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 EYRVRGSI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 EGEMRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=13429;
                                             NCBI_TaxID=13429;
                                                                                                                                  patterns.";
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ID 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 DLEGVAGERREBILLGMDPLENAISALWISNL--NQORALARSLIVVIQMVAEAVRFRFI 174
                                                                                                                                                                                                                                                                                                                                                                                                                           "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant 0.12:125(101997).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL, U76524; AAC15886.1; --
HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                          7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
RIBOSOME INACTIVATING PROTEIN, A CHAIN.
RIBOSOME INACTIVATING PROTEIN, B CHAIN.
; 3ED286C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukarocas, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                       Query Match

38.4%; Score 395.5; DB 10; Length 549;
Best Local Similarity 50.0%; Pred. No. 1e-28;
Matches 94; Conservative 27; Mismatches 60; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last amotation update)
Ribosome inactivating protein precursor (EC 3.2.2.2) (TRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Damme B.J., Roy S., Barre A., Rouge P., Van Leuven F.,
                                                                                                                                                                                                                          02607FE607CA44B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSS0231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO00772; Ricin_B_lectin.
InterPro; IPRO01574; RIP.
Bean; PRO0652; Ricin_B_lectin; 6.
Pfam; PRO0161; RIP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
                                                                            PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-glycosidase).
Sambucus nigra (European elder)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62336 MW;
InterPro; IPR001574; RIP. ___
Pfam; PF00652; Ricin B lectin;
Pfam; PF00161; RIP; I.
                                                                                                                                                                                                1 1
549 AA; 60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PR00396; SHIGARICIN.
SM00458; RICIN; 2.
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 EYRVRGSİ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 EGEMRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 AA;
                                                                                                                                                                           Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peumans W.J.;
                                                                                                                                                                                                                             SEQUENCE
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125 DRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTOLPTLARSFIICIQMISEAARFQY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, M98346, AAA32626.1; -.
HSSP, P11140, 1ABR.
INTERPRO, IPR000772, Ricin B lectin.
InterPro, IPR01574; RIP.
Pfam, PF00652, Ricin B lectin, 6.
Pfam, PF00161; RIP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q94KE4, PRELIMINARY; PRT; Q94KE4; (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                01, Created)
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0396; SHIGARICIN.
MART; SMO0458; RICIN, 2.
PROSITE; PS50211; RICIN B LECTIN;
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Conservative
                                                                                                                                                                                               PRELIMINARY;
                                                                        185 IEGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 SNRVGVSİR 180
                                                                                                      195 İEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 EGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase, Toxin.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3816;
                                                                                                                                                                                                                                01-NOV-1996
01-NOV-1996
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ID 09
AC 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                           67 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 124
                                                                                                                                                                   DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 184
                                                                                                                                                                                                                                      7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 YPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVOVKNRFVLVRLTNY 87
                                                                            99
                                                                                                       28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVOVKNRFVLVLLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin l.";
Submitted (AFR-2000) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-- SIMILARITY: ASSON TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match
33.8%; Score 347.5; DB 10; Length 564;
Local Similarity 41.1%; Pred. No. 3.6e-24;
hes 78; Conservative 41; Mismatches 56; Indels 15; Gaps
                                                                        7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Asteridae, campanulids; Dipsacales; Adoxaceae, Sambucus.
                                        15;
         DB 10; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
8-glosome-inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).
     34.1%; Score 350.5; DB 10; Length 41.6%; Pred. No. 1.9e-24; ive 40; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
; 8261681A6DB55CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS, PROGUS, SHIGARICIN.
SMART; SMO0458; RICIN, 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS60275; SHIGA RICIN; 1.
Glycosidase; Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P02879; ZAAI.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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564 AA; 62694 MW;
                                            79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                           185 IEGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                             195 İEQEVRRSLQ 204
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=28503;
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126 RIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIOMASEAARYRCI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93132789; PubMed=8421313; MEDLINE=93132789; PubMed=8421313; MEDLINE=93132789; PubMed=8421313; MEDLINE=93132789; PubMed=8421313; MEDLINE=93132789; PubMed=84.0.°C., Lin J.-Y.; Medlines sequencing conservation and significance."; J. Mol. Biol. 229:263-267(1993).

-! AMOI. Biol. 229:263-267(1993).
-! CATALYIC ACTIVITY: ENDONDROROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.
-! SIMILARITY: NELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TERMBLrel. 01, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.22) (TRNA N-glycosidase) (Fragment).
Abrins precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Pabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QYPIINFTTAGATVQSYTNFIRAVRGRLFTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%; Score 344.5; DB 10; Length 528; 45.0%; Pred. No. 6.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 528
528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;
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Pfam; PF00161; RIP; 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 IISVAIDVINVYIMGYRAGDISYFĘ---NEASAITEAAKYVFKDSMRKIILPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AB039324; BAA92530.1; --
                                                                                                                                                                                                                                                                     Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF367252; AAK52960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes
                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
01-DEC-2001 (TrEMBLrel. 19; Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AA; 31706 MW; A6D5602549CA5657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 340; DB 10;
39.5%; Pred. No. 7.2e-24;
tive 46; Mismatches 54;
                                                                                                        Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRICHOSANTHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
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InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=118182;
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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Q9LRE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 IISVAIDVINVYVMGYRAGDISYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=94271613; PubMed=8003348;

MEDILINE=94271613; PubMed=8003348;

Zheng H., Wang B., Shaw P., Yeung H.;

[Cloning and DNA sequencing of the gene encoding trichosanthin].";

I Chuan Haueh Pao 21:42-51(1994).

-! - CATALYTIC ANDIAVYROKOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RURA.

-! - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
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Trichosanthes kirilowii (Mongolian snake-gourd).
Trichosanthes kirilowii (Mongolian snake-gourd).
Trichosanthes kirilowii (Mongolian snake-gourd).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                y Match 32.8%; Score 338; DB 10; Length 289; Local Similarity 39.5%; Pred. No. 1.1e-23; hes 73; Conservative 46; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                    Query Match 32.8%; Score 338; DB 10; Length 247; Best Local Similarity 40.0%; Pred. No. 8.9e-24; Matches 74; Conservative 46; Mismatches 53; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
                                                                                                            247 247
247 AA; 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
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PROSITE; PS00275; SHIGA_RICIN; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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HSSP; P09989; 1MRJ.
InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 MRTRI 193
                                                            Hydrolase; Toxin.
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us-10-083-336a-10.rspt

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           177 GVSİR 181
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                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
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129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                ONE
                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT C SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- STBUNIT: DISULEDE-LINKED DIMEN OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOWAIN CONSISTS OF 3 HOMOLOGUIS SUBDOMAINS (ALPHA, BETA, GANWA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.
EMBL, X54872; CAA3865411; --
HSSP; P11140; LABR.
                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 266:6848-6852(1991).
-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                 Evensen G., Mathiesen A., Sundan A., "Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00161; A.F., ..
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; ABRIN E, A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.7%; Score 336.5; DB 10; Length 252; 44.9%; Pred. No. 1.3e-23; tive 24; Mismatches 69; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update).
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment)
                                                                                                                                                                                                                                                        Abrus precatorius (Indian licorice) (Crab's eye)
                                                                                                                                                         252 AA.
                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                           TISSUE=LEAF;
MEDLINE=91201329; PubMed=2016300;
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Pfam; PF00161; RIP; 1.
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                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 2
252 AA;
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Best Local Similarity
Matches 83; Conserv
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                                                                                   194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                          189 MRTRI 193
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3816;
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                                                                                                                                RESULT 12
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ID Q3
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88 NGNIVITAVDVINLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins from Sambucus nigra leaves.";
Submitted (AUG-2010) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 268 RRNA.
-- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF409132; ALGIN B. Jectin.
InterPro; IPR001574; Ricin_B lectin.
Fram: PF00652; Ricin_B lectin; 6.
Pfam; PF00652; Ricin_B lectin; 6.
Pfam; PF00165; Ricin_B lectin.
FRINTS; RR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization and cloning of lectins and ribosome-inactivating
                                                                                                                                                                                                                      Sambucus nigra (European elder).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopernatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.

NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%; Score 330.5; DB 10; Length 563; 39.5%; Pred. No. 1.4e-22;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin l precursor
(BC 3.2.2.2) (Buropean elder)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Toxin.
SEOUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
                        Q945S2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein (EC 3.2.2.22) (TRNA
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563 AA
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PRT;
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Best Local Similarity 39...
best Tocal Similarity
Tocal Similarity
Tocal Similarity
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 IEGEMRTRIR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Damme E.J.M.;
                                                                                                                                                                       N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Leaf
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Glycosidase; Hydrolase; Toxin.

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125 DRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFOY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 66
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Chin-Hung H., Lee M.C., Chen J.X., Lin J.Y.,

"Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.",

Bur. J. Biochem. 219:83-87(1994).

-! CATALYIT: ENDOHYBOLYSIS OF THE N-GLYCOSIDIC BOND AI ONE
SPECIFIC ADENOSINE ON THE 268 RRAM.
-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL, X54873; CAA38655.1; -.
                                                                                                                                                                              TISSUE=Leaf;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
"Characterization and molecular cloning of Nigrin 1, a type two
"Characterization and molecular cloning of Sambucus nigra";
Tibosome-inactivating protein from leaves of elder (Sambucus nigra).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF249280; AAN86130.1; -.
Hydrolase; Glycosidase.
SEQUENCE 563 AA; 62173 MW; OEB236421FC5E04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota, Vüridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             % Match 32.1%; Score 330.5; DB 10; Length 563; Local Similarity 39.5%; Pred. No. 1.4e-22; les 75; Conservative 39; Mismatches 61; Indels 15;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         038761; Q96234;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ricin A-chain type 73 (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leaf;
Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA.
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PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X76720; CAA54138.1; -. HSSP; P11140; 1ABR.
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195 IEQEVRRSLQ 204
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                                                                                                                                                                               63
                                                                                                                                          10 INFTIAGATVOSYTNFIRAVRGRLITGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                             6 IKFSTEGAISQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE
                                                                                                                                                                                                                                         64 SIEVGIDVINAYVVAYRAGIQSYFLRDAPSSASD----YLFIGT-DQHSLPFYGTYGDL
                                                                                                       13; Gaps
                                                                Match 32.0%; Score 329.5; DB 10; Length 252; Local Similarity 42.8%; Pred. No. 5.8e-23; Local Solutive 28; Mismatches 66; Indels 13;
             252 252
252 AA; 28229 MW; 187B8B4E134AECE5 CRC64;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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1: /SIDS1/qcqdata/q
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	Description	Ricin A chain. Un	Ricin A-chain (RTA	Ricin A-chain ribo	Ricin A-chain RIP.	Ricin A. Escheric	Sequence of Ricinu	Ricin A encoded by	Anti-cataract immu	Ricin D. Ricinus
SUMMARIES	ID	AAR37290	AAR63902	AAW25136	AAW21699	AAP70097	AAP70838	AAP95639	AAR70827	AAP90079
	DB	14	16	18	18	æ	œ	10	16	10
	Query re Match Length DB I	267	267	290	290	332	332	332	554	562
oko	Query Match	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9
	Score	955	955	955	955	955	955	955	955	9 ዓ.
	Result No.		7	m	4	ß	9	7	00	σ

Sequence of prepro	Castor bean prepro	Modified castor be	Sequence of Ricinu	Castorbean ricin.	Castor bean ricin	Ricinus communis r		Castor bean prepro		Seguence of G-FIT.	Preproricin, Rici	Sequence of Ricinu	Ü	DNA sequence of ri	Ricin A from picil	Amino acid sequenc	gene ]	Ricin A chain (RTA		Castor oil plant a	R. communis agglut	Sequence of Ricin	Ricin agglutinin A	Trichosanthin anti	Amino acid sequenc	Synthetic alpha-tr	Mature alpha-Trich	œ.		Trichosanthin from	Trichosanthin from	Trichosanthin prot	Encodes chinese cu	Alpha-trichosanthi	Chinese cucumber a
AAP50166	AAG78300	AAG78304	AAP70326	AAW25787	AAY55892	AAY78592	AAG78301	AAG78302	AAR39570	AAR39571	AAP60240	AAP70325	AAP80164	AAP94793	AAR30722	AAB19265	AAR06554	AAR74176	AAR32430	AAW25143	AAW21706	AAP70324	AAP95648	AAR67359	AAY69048	AAR07518	AAR25573	AAW25140	AAW21703	AAR07514	AAR25572	AAR29272	AAR32986	AAR55129	AAW10468
9	22		œ	18	20	21	22	22	14	7	7	æ	σ	10	13	21	11	16	14	18	18	œ	10	16	27	1	13	18	18	11	13	13	14	15	18
565	265	265	576	576	216	576	576	576	268	534	265	574	200	574	267	267	332	267	267	540	540	534	280	247	247	248	248	267	267	289	289	289	289	289	289
	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	7.76	97.4	97.4	97.2	97.1	97.0	6.96	96.9	8.96	96.2	94.6	88.8	88.8	82.6	74.1	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5
955	955	955	955	955	955	955	955	955	953	950	950	948	947	946	945	945	944	938	922	ın	865.5	ın	722	336	336	336	336	336	336	336	336	336	336	336	336
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## ALIGNMENTS

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Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
                                                                                                                                                                                                                                              Lei SP;
                                                                                                                                                                                                                                              Carroll SF, Lane JA,
                 AAR37290 standard; protein; 267 AA.
                                                                                                                                                                                  92WO-US09487.
                                                                                                                                                                                                   91US-0787567.
92US-0901707.
                                                                   (first entry)
                                                                                                                                                                                                                                               serhard SL, Better MD,
                                                  (updated)
(updated)
                                                                                                                                                                                                                                                               WPI; 1993-167617/20.
                                                                                                                                                                                                                             (XOMA ) XOMA CORP.
                                                                                    Ricin A chain.
                                                                                                                                                                                   04-NOV-1992;
                                                  25-MAR-2003
09-JAN-2003
13-SEP-1993
                                                                                                                                               WO9309130-A1.
                                                                                                                                                                                                    04-NOV-1991;
19-JUN-1992;
                                                                                                                               Unidentified
                                                                                                                                                                 13-MAY-1993.
                                 AAR37290;
RESULT 1
         AAR37290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELSNHAELSVILALDVINAYVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYFFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                               The invention covers analogues of Type I RIPs. Ricin is a Type II RIPs whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment.

(Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                       ---VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                       10; Gaps
Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) encoding type I ribosome-inactivating proteins
                                                                                                                                                                                                                                                                                                                                                   97.9%; Score 955; DB 14; Length 267; 95.0%; Pred. No. 3.7e-94; tive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A chain, RTA, ribosome-inactivating proteins; RIPs, cytotoxic therapeutic agents; autoimmune disease; cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                        2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR63902 standard; protein; 267 AA
                                                                       Claim 1; Page 92; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FOYIEGEMRTRIRYNRRSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US05348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                       Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll SS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricin A-chain (RTA)
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                     267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1993;
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                        Query Match
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1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 BLSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SIT-1; Luffin A; MARP; Ricinus communis agglutinin; Momordin; PAP-S, fuffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                  Indels 10; Gaps
                                                                              AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPs) described in AAR63903-R63911. RIPs are the key components of cytcoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin A-chain ribosome inhibitory protein inactive precursor.
                                                                                                                                                                                                                                                                                                                           Query Match

97.9%; Score 955; DB 16; Length 267;

Best Local Similarity 95.0%; Pred. No. 3.7e-94;

Matches 189; Conservative 0; Mismatches 0; Indels 10
which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                   2 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLT----
                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW25136 standard; Protein; 290 AA.
                                                   Example 3; Fig 1; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 FOYIEGEMRTRIRYNRRSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0987927.
90US-0535636.
95US-0378761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                  therapeutic agents.
                                                                                                                                                                                                                                                                                                267 AA;
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26-JAN-1995
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                                                                                                                                                                                                                                                  disease
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pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                       Claim 4; Column 91-94; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW21699 standard; Protein; 290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  172 FOYIEGEMRIRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                   205 FOYIEGEMRIRIRYNRRSA 223
       Walsh TA;
                                                                                                                                                                                                                                                                        95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                  Matches 189; Conservative
       Morgan AER,
                       WPI; 1997-362934/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricin A-chain RIP.
                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                   290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis.
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172 FOYIEGEMRTRIRYNRRSA 190
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                                                                                                                                                                                                                                                                                     Walsh TA;
                                                                                                                                  95US-0378761.
                                                                                                                                                                       92US-0987927.
                                                                                                                                                                                       90US-0535636.
95US-0378761.
                                                                                                                                                                                                                                                                                       Hey TD, Morgan AER,
                                                                                                                                                                                                                                                                                                                            WPI; 1997-309831/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 AA;
                                                                                                                                                                                                                                                 (DOWC ) DOWELANCO.
                                                                                                                                                                                           11-JUN-1990;
26-JAN-1995;
                                                                                                                                  26-JAN-1995;
                                                                                                                                                                         09-DEC-1992;
                                                        US5635384-A.
                                                                                              03-JUN-1997
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                                                                                                                                                                                                       AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and bete units of the RIP. When
engared the two units regain and bete units of the RIP. When
exparated the two units regain and are capable of inactivating
cukaryotic ribosomes and hence preventing protein production. Many
different RIPs may be produced with an internal linker including
maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as the
tatachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see US4869903). There is interest
in expressing RIP recombinantly in host cukaryotic cells, because of
the capacity to provide correct post-translational processing. However,
RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
in cell death. Since the inactive RIP proteins are not cytotoxic to
then converted to active RIP proteins are not cytotoxic to
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GNYDRLEQLAGNLRENIELGNGPLBEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                              precursors of ribosome inactivating proteins, can be expressed in eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 955; DB 18; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                  encoding pro-ribosome inactivating proteins - inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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The sequences given in AAW21698-710 represent Ribosome Inactivating
Proteins (RIP's), which may be used in the construction of the
Proteins (RIP's), which may be used in the construction of the
proxIP of the invention. The proxIP has a selectively removable,
contennal peptide linker. The precursor sequence is incapable of
inactivating eukaryotic ribosomes, but can be converted by removal
of the linker into a protein having alpha and beta fragments and being
capable of inactivating eukaryotic ribosomes. RIPs are potent
inhibitors of eukaryotic protein synthesis. They possess a highly
specific N-glycosidae activity which cleaves the glycosidic bond of
adenine 4324 of rat liver ribosomal 285 RNA. RIP's selectively inhibit
cellular proliferation of cells, e.g. cancer cells and HIV-infected T
cells. The inactive prokIP proteins make it possible to provide protein
synthesis inhibitors with uses in practical and improved ways not before
possible. The RIP can be used to make cytocoxic conjugates.
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/note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inactive precursor of maize ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing internal linker sequences
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Best Local Similarity 95.0%; Pred. No. 4.1e
Matches 189; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Column 91-94; 121pp; English.
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(updated)
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                                                                                                                          (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
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Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 332 AA;
                                                                                                                                                                                                N-PSDB; AAN70519
                                                                                                     07-MAR-1986;
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31-OCT-2002
                                                                             13-NOV-1986;
                                EP237676-A.
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                                                                                                                                                             Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ELSNHARISVTLALDVINAYVVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYYFRAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 ELSNHARELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                   2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
A protein encoded by pRA123.
                                                                                                                                                                                                                                    N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                                          Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 955; DB 8; Length 332;
95.0%; Pred. No. 4.9e-94;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                           Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70838 standard; protein; 332 AA
                                                                                                                                                                           Chang S,
                                                                                                                                                                                                                                                                      Disclosure; Fig. 4; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 FOYIEGEMRIRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 FOYIEGEMRTRIRYNRRSA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Leader"
  Ricin A; Met-aminopeptidase.
                                                                                             86EP-0307242.
                                                                                                                  86US-0860330.
85US-0778414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Matches 189; Conservative
                                                                                                                                                                            Bauer KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
                                                                                                                                                                                                  WPI; 1987-110172/16.
                                                                                                                                                  (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricinus communis.
                         Escherichia coli
                                                                                                                                                                                                               N-PSDB; AAN70152
                                                                                                                                                                            Benbassat A,
                                                                                             19-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant toxin.
                                                                                                                   36-MAY-1986;
                                                                                                                             20-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1991
                                                                      22-APR-1987.
                                                EP219237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP70838;
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtted. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see Inbrary was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70522) shows the nucleotide sequences of three plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression (AAN70523) and suitable retroregulators. (AAN70523) and suitable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non-glycosylated ricin precursor and toxin etc. - are prepd.
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.9%; Score 955; DB 8; Length 332; larity 95.0%; Pred. No. 4.9e-94; Conservative 0; Mismatches 0; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQYIEGEMRTRIRYNRRSA 234
/note="A-chain"
315..332
                                                                               /note="B-chain"
                                                                                                                                                                                                                                                                                                                     86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                    86US-0837583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purer and soluble prods.
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RESULT 6 AAP70838

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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the rimmunotoxin was expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 10; Gaps
                                                                                                                                                                                                     Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.9%; Score 955; DB 16; Length 554; Best Local Similarity 95.0%; Pred. No. 9.9e-94; Matches 189; Conservative 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                   28..145
/label= HEAVY
/note= "WAb 4197X heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood MS;
                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
/note= "phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wallace TL,
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                       AAR70827 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOUS-) HOUSTON BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig.4; 68pp; English.
 172 FOYIEGEMRIRIRYNRRSA 190
             216 FOYIEGEMRIRIRYNRRSA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= RICIN-A
                                                                                                                                                                                                                                                                                                                                                                             148..166
/label= LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0101329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549.:554
/label= TAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US07919.
                                                                                                                                                        (first entry)
                                                                                                                                                                                 Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                          276..544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gould RM, Kelleher PJ,
                                                                                                                                           (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ85386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9503828-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1993;
                                                                                                                                         25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1995
                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                 AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid RA123 (ATCC No. 19799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                            Greenfield L, Nitecki D, Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 955; DB 10; Length 332; 95.0%; Pred. No. 4.9e-94; tive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host cells.
(Updated on 31-OCT-2002 to add missing OS field.)
(Updated on 25-MAR-2003 to correct PF field.)
(Updated on 25-MAR-2003 to correct PR field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                                Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                         Ricin A encoded by insert from plasmid pRA123.
                                                                                                                                        /label= leader sequence
                                                                                                             iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Horn G,
                                                                                                                                                                     ...cnair
303..314
/label=linker
315..332
                                                                                                                                                    36..302
/label=A-chain
                                                                                                                                                                                                        315..332
/label=B-chain
                                                                                                                                                                                                                                                                                                                     84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                                                                                              89EP-0201162
                                                                                                                                                                                                                                                                                                                                                                                                  (CETU ) CETUS CORPORATION.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Lawyer FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA;
                                                                         Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN91281
                                                                                                                                                                                                                                                                                                                     08-FEB-1984;
08-FEB-1984;
09-FEB-1984;
07-SEP-1984;
20-SEP-1984;
13-AUG-1990
                                                                                                                                                                                                                                                                                              19-JAN-1989;
                                                                                                                                                                                                                                                                      04-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                           Gelfand D,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Piatak MJ;
                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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96 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQBDAEAITHLFTDVQNRYTFAFG
                                         112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
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                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                  AAP50166 standard; Protein; 565 AA
                                                                                                   172 FOYIEGEMRIRIRYNRRSA 190
                                                                                                                        FOYIEGEMRTRIRYNRESA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamb FI;
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/label= signal
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83CH-0019265.
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                                                                                                                                                                                                                                                                                                               roxin; anti-tumour therapy
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              25..565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYWA-) UNIV WARWICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1985-148040/25.
N-PSDB; AAN50202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-1984;
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                                                                                                                                                                                                                                                         16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP145111-A.
                                                                                                                                                                                                                              AAP50166;
                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                           Ricinus
                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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       ---VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                   GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                      338 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAFG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                   Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 955; DB 10; Length 562; 95.0%; Pred. No. 1e-93; 1ive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT--
                                                                                                                                                                                                                                                                          AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, fig 1; 51pp; English.
                                                                                                                                                                                              172 FOYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricinus communis (caster beans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0124735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88WO-US04238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189; Conservative
                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN90068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8904839-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1989.
                                                                                                                                                                                                                                                                                                                                              01-NOV-1989
                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                      112
                                                                52
                                                                                                                                                                                                                                                                                                                                                                           Ricin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Dp

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preproricin is the whole polypeptide encoded by AANS0202 and the DNA encoding this is claimed. Prozicin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292..303
/label= links the C-terminus of the A chain and
the N-terminus of the B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequences coding for ricin type plant toxin - mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438..440
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398..400
/label= N-linked glycosylation
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/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label = N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of preproricin encoded by pRCL617.
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Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                             AAG78304
                                                                                                                                                                                                                                                                                                                                                                                                             HILLILLILLILLILLILLIK SOOKKAKKKE KACKACK
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                                                                                                                                     112 GNYDRIEQIAGNIENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                            145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                              21
                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 .565
|Jabel= Ricin B_chain
|note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                             25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGKLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                              ---VLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                 Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                             Gaps
                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Linker peptide
/note= "Cleaved during activation of ricin"
                        Score 955; DB 6; Length 565;
Pred. No. 1e-93;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Castor bean preproricin protein (SEQ ID 1).
                                                              2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47-50; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     25..290
/label= Ricin A chain
/note= "N-glycosidase"
291..302
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                           AAG78300 standard; Protein; 565 AA.
                                                                                                                                                                                            205 FOYIEGEMRIRIRYNRKSA 223
                                                                                                                                                                           172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2000; 2000US-0182759.
                           97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                                (first entry)
                                            Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keener WK, Ward TE;
                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI64137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus infection.
                                                                                                                                                                                                                                                                                                                                                          Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200160393-A1
                                                                                                                                                                                                                                                                                15-NOV-2001
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                                                                                                                                                                                                                                                             AAG78300;
          Seguence
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                   AAG78300
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The sequence relates to preproricin protein encoded by the DNA sequence given in AA164137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The invention is useful for treating human immunodeficiency virus infected and other viral genome into the host genome thereby preventing the integration of the viral genome into the host genome thereby preventing the integration of the viral genome into the host genome thereby preventing the class those to act as host cells for the virus. The artiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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/label= Proricin
/note= "Proricin consists of the ricin A chain, a linker
peptide, and the ricin B chain. Proricin is
proteolytically cleaved between the A chain and
the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.9%; Score 955; DB 22; Length 565; Best Local Similarity 95.0%; Pred. No. 1e-93; Matches 189; Conservative 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..24
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosidase"
292..303
/label= Linker_peptide
296..297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78304 standard; Protein; 565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 FOYIEGEMRIRIRYNRKSA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 AA;
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25-MAR-2003
                                                                                                                                                      Region
                                                                                                                                                                              Region
                                                                                                                                                                                                      Region
ద
                                                                                                                                                                                                                                                                                                                               The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AA164145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and viruside activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the latency/rebound viral genome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNOEDAEAITHLFTDVONRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                       composition comprising toxin e.g., ricin based antiviral compound for treating viral infections such as human immunodeficiency
             304..565
|Jabel= Ricin B chain
|note= "Galactose/N-acetylgalactosamine-binding lectin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 97.9%; Score 955; DB 22; Length 565; Local Similarity 95.0%; Pred. No. 1e-93; hes 189; Conservative 0; Mismatches 0; Indels 10
  'label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                           Example 1; Page 59-63; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 FOYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                  15-FEB-2001; 2001WO-US05282
                                                                                                                                           16-FEB-2000; 2000US-0182759
                                                                                                                                                                                             Keener WK, Ward TE;
                                                                                                                                                                                                                     2001-581908/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 AA;
                                                                                                                                                                                                                                 N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                    virus infection.
                                                                 WO200160393-A1
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Matches
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AAP70326 standard; Protein; 576 AA.

AAP70326;

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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin B (AAN70526) and RCA (AAN70524) in precursor for form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521), shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression (AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%; Score 955; DB 8; Length 576; 95.0%; Pred. No. 1e-93; tive 0; Mismatches 0; Indels 1
                                                                                                                                                                       Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                               Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 14(1-2); 112pp; English.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "A-chain"
315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "B-chain"
                                                                                                                                                                                                                                                                                                                                                                  1..35
/note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86EP-0308877.
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(updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           36..302
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                                                                                                                                                                                                                                                                      Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN70526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1987.
                                                                                     Sequence of
                                                                                                                                                                                                          plant toxin
                               21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP237676-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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156 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see AAT91638) encoding the enzymatic A domain and a portion
of the A-to-B linker peptide of ricin was used to construct a
ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in
E. coli. The hybrid protein can be isolated and used to treat
conditions involving over-production of cells bearing IL2 receptors,
such as certain T-cell lymphomas and organ transplant rejection
crises. The hybrid inactivates ribosomes in cells bearing IL2
receptors, resulting in cessation of protein synthesis and death of
target cells. Claimed hybrid proteins comprise a translocation
domain and a cell binding domain from e.g. a hormone, growth factor
or polypeptide toxin. The hybrid molecules can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a
                                                                                                                                                                                                 Ricin, cytotoxin, hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                               1..35
/label= Sig_peptide
36..302
/label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 11A-B; 30pp; English
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                  AAW25787 standard; Protein; 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                               315..576
/label= B-domain
                        FOYIEGEMRTRIRYNRRSA 190
                                         216 FOYIEGEMRTRIRYNRRSA 234
                                                                                                                                                                                                                                                                                                                           303..314
/label= Linker
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                                                                                                                                            (updated)
(first entry)
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                                                                                                                                                                                                                                               Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT91638
                                                                                                                                                                              Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1991;
07-JUN-1984;
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22-DEC-1989
                                                                                                                                            25-MAR-2003
27-MAR-1998
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                        172
                                                                                                                      AAW25787;
                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                        AAW25787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane, HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                           36 İFPKQYPİİNFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                2 IFPKQYPIINFTTAGATVQSYTWFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                10; Gaps
delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                          97.9%; Score 955; DB 18; Length 576; 95.0%; Pred. No. 1e-93; ive 0; Mismatches 0; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY55892 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 FOYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 FOYIEGEMRTRIRYNRRSA 234
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84US-0618199.
91US-0722484.
85US-0726808.
85US-0742554.
89US-0456095.
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Matches 189; Conservative
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                                                                                                                                                                                                                                               576 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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22-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY55892;
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                  Query Match
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                  8888888888888
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Example 4; Fig 11; 31pp; English. \$

The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein coxin, Tr toxin, Shiga-like toxin, pertussis toxin and tetamus coxin, which translocate the third part of the across the cytoplasmic toxin, which translocate the third part of the across the cytoplasmic comprise into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-mative to the naturally occurring protein of (b). This sequence represents the castor bean rich toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and calleviate or cure the disease. The hybrid is especially used in treating energy particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected.cells!), to counteracting viral infections such as complying the missing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as complying the missing detains on the process of getting non-therapeutic substances such as construction in the process of getting non-therapeutic substances such as construction in the process of getting non-therapeutic substances such as constructions.

576 AA; Sequence

1; Query Match
97.9%; Score 955; DB 20; Length 576;
Best Local Similarity 95.0%; Pred. No. 1e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps

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156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215 112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171 셤 ö

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Search completed: February 10, 2004, 16:22:29 Job time : 32.3944 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:18:30; Search time 10.9859 Seconds (without alignments) 731.761 Million cell updates/sec Run on:

US-10-083-336A-11

975 1 MIFPKQYPIINFTTAGAIVQ......RFQXIEGEMRTRIRYNRRSA 190 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:\*

1. /ogn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2. /ogn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

3. /ogn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4. /ogn2\_6/ptodata/1/iaa/PGTUS\_COMB.pep:\*

5. /ogn2\_6/ptodata/1/iaa/PGTUS\_COMB.pep:\*

5. /ogn2\_6/ptodata/1/iaa/PGTUS\_COMB.pep:\*

6. /ogn2\_6/ptodata/1/iaa/PGTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	æ	Sequence 10, Appl	ř	'n	'n	Ļ	Ļ	'n	'n	٦,	Sequence 1, Appli	'n	27	27	Ω̈́	16,	61	ř	77	77,	ģ	9	Ġ	ý	Sequence 6, Appli	equence 6, Appl	Sequence 74, Appl
	ID	-08-356-78	-08-356	-07-901-70	-988-43	-08-425-	US-08-488-113B-1	77-484B	-646-360-	US-08-839-765-1	- 1	US-09-610-838-1	S92-	8-761A-	US-08-485-286-27	5248606-4	US-08-218-303-16	US-08-338-793D-61	US-09-538-873-1	-,	US-08-485-286-77	US-08-488-113B-6	US-08-477-484B-6	US-08-646-360-6	US-08-839-765-6	US-09-136-389-6	US-09-610-838-6	US-08-378-761A-74
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Indels 10;

Query Match 98.5%; Score 960; DB 2; Length 268; Best Local Similarity 95.0%; Pred. No. 2.5e-103; Matches 190; Conservative 0; Mismatches 0; Indels 1

74, Appl 4, Appli 4, Appli 4, Appli 4, Appli 4, Appli 15, Appli 6, Appli 6, Appli 6, Appli 6, Appli 7, Appli 8, Appli 8, Appli 8, Appli 8, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 1,	
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US-08-485-286-74 US-07-923-692C-4 US-08-184-237-4 US-08-484-920-4 US-08-483-502-4 US-08-483-502-4 US-09-72-6-51A-4 US-09-72-6-51A-4 US-08-324-301-15 US-07-901-707-6 US-08-922-09487-7 US-08-922-09487-7 US-08-922-09487-7 US-08-922-09487-7	
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336 336 336 336 336 310.5 310.5 310.5 305 305 305 305 305 303 303	
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# ALIGNMENTS

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APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
ITILE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
ADDRESSE: Edward R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION 424
FILORASIFICATION DATA:
APPLICATION NUMBER: 07/831,967
FTILING DATE: 0.6-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRP-053
                                             Sequence 8, Application US/08356786 Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INPERATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 268 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                 GENERAL INFORMATION:
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RESULT 1
US-08-356-786-8
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us-10-083-336a-11.rai

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123 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 182
63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
                                              111 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.9%; Score 955; DB 1; Length 267; 95.0%; Pred. No. 9.4e-103; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PROM APPLICATION TOWNER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTONNEY/AGENT INPOMERATION:
NAME: NO. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                 171 RFQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                            183 RFQYIEGEMRTRIRYNRRSA 202
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07901707 Patent No. 5376546
                                                                                                                                                                                                                                                                                                                                                     Bernhard, Susan L.
Better, Marc D.
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 189; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 267 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bernha
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                      VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 110
                                                                                                                                 61 VELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                                                                                                               111 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 MIFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 62
                           1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
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Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Hopermann, Hermann
APPLICANT: House ton, L. L.
APPLICANT: House, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
ITILE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R. Pitcher, Testa, Hurwitz, & Thibeault
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98.5%; Score 960; DB 2; Length 534;
Best Local Similarity 95.0%; Pred. No. 6.8e-103;
Matches 190; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exchange Place, 53 State Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALF: CALCA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 10:
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amino acid
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MOLECULE TYPE: protein
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Massachusetts
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ADDRESSEE: Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAX-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-36,989
                                                                                                                                                                                                                                 Sequence 1, Application US/08425336
Patent No. 5621083
                                                                                        172 FOYIEGEMRIRIRYNRRSA 190
                                                                                                                                181 FOYTEGEMRTRIRYNRRSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Thomas C. REGISTRATION NUMBER: P-3(REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
1 IFPRQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTOONEY/AGENT INFORMATION:
NAME: NO: 5416202and, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31133 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               Sequence 1, Application US/07988430 Patent No. 5416202
                                                                 172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                       181 FOYIEGEMRTRIRYNRESA 199
                                                                                                                                                                                                                                                                                     APPLICANT: Bernhard, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (312) 346-5750
(312) 984-9740
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-07-988-430-1
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                US-07-988-430-1
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APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxine Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.9%; Score 955; DB 1; Length 267; 95.0%; Pred. No. 9.4e-103; tive 0; Mismatches 0; Indels 1
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60661
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                                                                                                                                                                                                                                                                                                                                 US-08-477-484B-1
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1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                            Sequence 1, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%; Score 955; DB 1; Length 267; 95.0%; Pred. No. 9.4e-103; live 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                181 FQYIEGEMRTRIRYNRRSA 199
                                                                 172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
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TELEFAX: 312/707-9155
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Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Chicago
STATE: Illinois
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 1111
                                                                                                    112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Better, Marc D.
APPLICANT: Carcoll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
STREEP MCANDENCE
STREEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 955; DB 1; Length 267;
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APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
PRIOR APPLICATION NUMBER: US 07/787,567
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08477484B Patent No. 5756699
                                                                                                                                                                                                             172 FQYIEGEMRTRIRYNRRSA 190
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,91
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                    61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 120
                                                                                                                                                                                                                                                                       GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                             -----VLPNRVGLPINQRFILV 51
                                                                                                    1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Standnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
                            10;
                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
WIRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
  Pred. No. 9.4e-103;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                        2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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APPLICATION NUMBER: PCT/US94/05348
APPLICATION NUMBER: PCT/US94/05348
FRING APPLICATION NUMBER: US 08/064,691
FRING APPLICATION NUMBER: US 08/064,691
FRING APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FRING APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FRING APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FRING APPLICATION DATA:
APPLICATION NUMBER: US 07/97,567
FRING APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FRING APPLICATION NUMBER: US 07/787,567
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
BERGISTRATION NUMBER: 32,918
BERGISTRATION NUMBER: 33,918
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
95.08;
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  Best Local Similarity 95.03
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: IC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60661
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GNYDRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                              1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                              ---VLPNRVGLPINORFILV
                                                                                                                                                                           Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
                                                                                                                             Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 12-APR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: US 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: US 07/988,430

FILING DATE: US 07/988,430
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                                                                                                                        Score 955; DB 2; I
Pred. No. 9.4e-103;
0; Mismatches 0;
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTATION NUMBER: 32,918
REFERENCE, DOCKET NUMBER: 11022US09/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 FQYIEGEMRTRIRYNRRSA 190
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                                                                                                                           97.9%;
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MEDIUM TYPE: Floppy disk
                                                                                                                     Query Match
Best Local Similarity 95.0°
Matches 189; Conservative
                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-1
amino acid
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                              52 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09136389
Patent No. 6146850
Patent No. 6146850
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF ENVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   Length 267;
                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                            Query Match 97.9%; Score 955; DB 3; I
Best Local Similarity 95.0%; Pred. No. 9.4e-103;
Matches 189; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-UUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
  312/707-8889
                                                                                                                                                                                 MOLECULE TYPE: protein
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STREET: Sov
CIIY: Chicago
STATE: Illinois
                                                                                                                                                              linear
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CLASSIFICATION:
TELEPHONE:
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                                                                                                                                                         TOPOLOGY:
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US-09-136-389-1
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52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILV 51
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APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDIEWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 955; DB 3; Length 267; 95.0%; Pred. No. 9.4e-103; tive 0; Mismatches 0; Indels
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 FQYIEGEMRTRIRYNRRSA 190
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Patent No. 6376217
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                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAK: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 267 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 3113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 FQYIEGEMRTRIRYNRRSA 190
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           IBM PC compatible
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TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 267 amino acids TYPE: AMINO ACID
                                                                                                                19921104
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; MOLECULE TYPE: protein
PCT-US92-09487-1
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                                                                                                             FILING DATE: 1:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 955; DB 4; Length 267; 95.0%; Pred. No. 9.4e-103; tive 0; Mismatches 0; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                 NAME: MCMicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                               APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATMONEY/AGENT INFORMATION:
NAME: MANNIAL-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9209487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 FQYIEGEMRTRIRYNRRSA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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: Illinois
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Sequence 27, Application US/08378761A
Patent No. 563534
GENERAL INFORMATION:
PAPLICANT: WALSH, TERENCE A
APPLICANT: MALCH ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
CORRESPONDENCE ADDRESS:
ADDRESSE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY, INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 267;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.9%; Score 955; DB 5; L
Best Local Similarity 95.0%; Pred. No. 9.4e-103;
Matches 189; Conservative 0; Mismatches 0;
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION WOMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION UDATA:
APPLICATION WUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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Search completed: February 10, 2004, 16:29:35
    ATTORNEY/AGENT INFORMATION:
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Matches 189; Conservative
                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Patent No. 5248606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:4:
; LENGTH: 290
                                                                                                                                                                                                                                                                      US-08-485-286-27
                                                                                                                                                                                                                                                                                                          Query Match
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Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

Batent No. 5646026

APPLICANT: HEV, TIMOTHY D

APPLICANT: HEY, TIMOTHY D

APPLICANT: MACSH, ALICE ER

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSTILLE ROAD

GITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GNYDRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHEDNQEDAEAITHLFIDVQNRYTFAFG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 955; DB 1; L
95.0%; Pred. No. 1.1e-102;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33621
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/485,286
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                                              LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.09
Matches 189; Conservative
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SOFTWARE:
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52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.9%; Score 955; DB 1; Length 290; Best Local Similarity 95.0%; Pred. No. 1.1e-102; Matches 189; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%; Score 955; DB 6; Length 290; 95.0%; Pred. No. 1.1e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
ADPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
                                                                        38272B
ALENCE BORUCKI, ANDREA A REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE GRARACTERSTICS:
LENGTH: 290 amino acids
TYPE: amino acid
TYPE: amino acid
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Job time : 10.9859 secs

Sun Feb 15 07:29:57 2004

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                                                                                                             February 10, 2004, 16:26:46; Search time 24:507 Seconds (without alignments) 1623.314 Million cell updates/sec
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Sequence 8, A
Sequence 5, A
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                                                                                                                                                                                                                                 1 MIFPKQYPIINFTTAGATVQ.........RFQYIEGEMRTRIRYNRRSA 190
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Sequence 2,
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Sequence 3,
Sequence 1,
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-083-336A-10
US-10-083-336A-8
US-10-083-336A-5
US-10-127-890-1
US-10-083-336A-1
US-10-083-336A-1
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US-09-792-793A-39
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US-10-083-336A-6
US-10-083-336A-4
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US-10-083-336A-9
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                                                                                                                                                                                                                                                                                                                                    801455 segs, 209382283 residues
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                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
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998.1
997.9
996.9
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996.5
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Sequence 6, Appli Sequence 39, Appl Sequence 4, Appli Sequence 34, Appli Sequence 34, Appli	Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli	- H H H H 7	204444	Sequence 105, App Sequence 1, Appli Sequence 259, App Sequence 255, App Sequence 255, App Sequence 251, App
US-10-127-890-6 US-10-375-209A-39 US-10-280-679B-4 US-09-792-793A-34 US-10-376-209A-34	US-10-282-935-3 US-10-480-796-3 US-10-127-890-7 US-10-127-890-4 US-10-127-890-5 US-03-347-064-2	US-10-127-890-107 US-10-127-890-107 US-10-127-890-106 US-10-127-890-110 US-09-765-527-247	US-10-127-890-2 US-10-127-890-99 US-10-127-890-100 US-10-127-890-101 US-10-127-890-103 US-10-127-890-103	US-10-127-890-105 US-10-074-596-1 US-10-074-596-1 US-09-765-527-259 US-09-765-527-253 US-09-765-527-251
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         Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Robert W
TITLE OF INVENTION: Rich Vaccine and Methods of Making and Using Thereof
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIFPKOYPIINFTTAGATVQSYTNFIRAVRGRLTVLDRRVGLPINQRFILVELSNHAELS
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                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Length 190;
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                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 975; DB 12;
100.0%; Pred. No. 1.1e-103;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 190; Conservative
                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TRIRYNRRSA 190
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US-10-083-336A-11
                                                                                                                                                                                                                                                         SEQ ID NO 11
LENGTH: 190
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121 GNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQYIEGEMRT 180
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                                                                                                                                                                  122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQYIEGEMRT 181
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APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Willard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPRENCE: PF452US (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DAIE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
        1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSV
                                                           62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA
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Best Local Similarity 95.0%; Pred. No. 6.1e-102;
Matches 190; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 REQYIEGEMRTRIRYNRRSA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.1
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US-10-083-336A-10
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                                                                                                                                                                                                                                   APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael B
APPLICANT: Byrne, Michael B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10083336A
Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Minnemacher, Michael P
APPLICANT: Wannemacher, Mobael P
APPLICANT: Wannemacher, Wobert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: F67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
UNMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 189;
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                                                                                                                                                            Sequence 6, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 189; Conservative
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ORGANISM: Ricinus communis
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181 TRIRYNRRSA 190
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                                                                                                      RESULT 2
US-10-083-336A-6
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LENGTH: 189
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LENGTH: 188
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g à d δ g à Dp 120

Indels 10; Gaps

Length 200;

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ATTORNEY/AGENT INFORMATION:
NAME: MONISCHOLAB, Janet M.
REGISTRATION NUMBER: 32, 918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-127-890-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 267 amino acids
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                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
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Matches 189; Conservative
                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                124 LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
TITLE OF INVENTION: Rich Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                   Gaps
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                                                                                                          Length 188;
                                                                                                                                                 0; Indels
                                                                                                     98.1%; Score 956; DB 12; L 100.0%; Pred. No. 1.6e-101; Live 0; Mismatches 0;
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Publication No. US20030166196A1
GENERAL INFORMATION:
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                                  ORGANISM: Ricinus communis
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                                                                                                                                             Matches 186; Conservative
                                                                                                   Query Match
Best Local Similarity
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                                                          US-10-083-336A-8
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LENGTH: 188
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52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
CAPADRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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APPLICATION NUMBER: US/10/127,890
FLING DATE: 23-Apr-2002
CLASSIFICATION: VÜNENOWIN-
PRIOR APPLICATION OF THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE T
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                                                      APPLICANT: UNPORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Mannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
SUPPRATE: Petentin Ver. 2.1
SEQ ID NOS: 15
SEQ ID NO 1
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APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Mannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 955; DB 12;
Pred. No. 1e-100;
0; Mismatches 0
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                       Sequence 1, Application US/10083336A Publication No. US20030181665A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.0%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Ricinus communis
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US-10-083-336A-1
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, ODAN
APPLICANT: SMALLSHAW, DOAN
APPLICANT: SMALLSHAW, DOAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
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APPLICANT: GHETIE, VTCTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FILE REFERENCE: UTSO: 603
61 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAFG 120
                                                                                                              63 SNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.9%; Score 945; DB 12; Best Local Similarity 94.9%; Pred. No. 4.9e-100; Matches 187; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10282935 Publication No. US20030143193A1 GENERAL INFORMATION:
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Publication No. US20040009148A1
GENERAL INFORMATION:
                                                                                                                                                                                                      172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                   181 FOYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 YIEGEMRTRIRYNRRSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 SNHAELSVTLALDVTNAXVVGYRAGNSAXFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICALION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                              Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                        96.9%; Score 945; DB 12;
94.9%; Pred. No. 4.9e-100;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.5%; Score 941; DB 12;
94.9%; Pred. No. 9.2e-100;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US/09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR PILING DATE: 1999-03-30
PRIOR PILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 YIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 YIEGEMRTRIRYNRRSA 199
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 187; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                 SEQ ID NO 1
LENGTH: 267
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                                                                                                                                                                                                                                                                                                               US-10-440-796-1
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123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 117
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                                                                                                                                                                                                                                                                                                               APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
UNDMER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Wannemcher, Robert W
APPLICANT: Wannemcher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.4%; Score 939.5; DB 12; Length 1
98.4%; Pred. No. 1.2e-99;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                             Sequence 9, Application US/10083336A, Publication No. US20030181665A1; GENERAL INFORMATION:
                                                   174 YIEGEMRTRIRYNRRS 189
                                                                                                      183 YIEGEMRTRIRYNRRS 198
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Best Local Similarity 98.44
Matches 185; Conservative
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LENGTH: 179
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APPLICANT: McDonald, John R.

APPLICANT: McDonald, John R.

APPLICANT: McCogins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTIN VAT. 2.0
SEQ ID NO 39
LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
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                                                     36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
     ---VLPNRVGLPINORFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 INFITAGATVOSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::| :|| || || || :| || || :| || 2 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.5%; Score 336; DB 10; Length 247;
Best Local Similarity 38.9%; Pred. No. 3.9e-30;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps
2 IFPKOYPIINFTTAGATVQSYTNFIRAVRGRLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GNYDRLEQLAGNLRENIELGNGPL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/09792793A Patent No. US20020168370A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |:
171 IGKRV 175
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 protein search, using sw model OM protein February 10, 2004, 16:17:35; Search time 10.2817 Seconds (without alignments) 1777.145 Million cell updates/sec Run on:

US-10-083-336A-11 Title: Perfect score:

975 1 MIFPKQYPIINFTTAGATVQ......RQYIEGEMRTRIRYNRRSA 190 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description		addlitinin precurso	rRNA N-qlycosidase	abrin-d precursor	abrin-c precursor	karasurin - Mongol	щ	karasurin C - Tric	abrin-b precursor	abrin (clone 7.2)	abrin-a precursor	beta-luffin - smoo	Smo	rRNA N-qlycosidase	rRNA N-glycosidase	agglutinin I precu	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	mistletoe lectin I	rRNA N-glycosidase	rRNA N-qlycosidase	rRNA N-qlycosidase	rRNA N-glycosidase		~	betavulgin'- beet	rRNA N-qlycosidase	rRNA N-glycosidase
ID	DT.Can	RICSAG	RLTZT	S32431	S16022	JU0393	JC5032	JC5606	S32430	C39761	TZLSA	S23519	JN0108	S22494	RLPUGG	S62627	825560	JC4840	JC4235	PD0018	JT0753	S28421	A39817	S17757	JE0401	T12573	JC4811	\$28542	828539
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Query Match	9 7 9	· œ	34.5	3	m	33.4	33.4	ω,	33.1	31.8	31.1	30.8	30.1	28.2	28.0	28.0	27.9	27.7	27.2	27.1	25.3	19.1	17.8	17.4	•	15.2	•	13.4	13.0
Score	95.5	865.5	336	327.5	327.5	326	326	326	323	310.5	303.5	300.5	293.5	274.5	273	273	272	270	265	264	CO.	186.5	174	170	æ	48	3	131	127
Result No.		1 (2)	e	4	r.	9	7	<b>c</b> co	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

rRNA N-glycosidase ribosome-inactivat rRNA N-qlycosidase	rRNA N-glycosidase rRNA N-glycosidase rRNA N-glycosidase	rana marac rana n-glycosidase rana n-glycosidase protein synthesis	rRNA N-glycosidase hypothetical prote shiga-like toxin I Shiqa toxin 2 subu	Shiga toxin 2 subu Shiga-like toxin I
S29931 S46239 S05205	S28541 RLOHG2 S17519	A58923 RLBH JC5848	S17932 S21940 I54695 E90779	G85640 S01032
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30 31 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	, w w w .	4 4 4 4 0 1 2 6	4. 4. 2.

# ALIGNMENTS

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A,Accession: A24041
A,Molecule type: DNA
A,Residues: 1-576 c4HL)
A,Residues: 1-576 c4HL)
A,Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083
B,Cross-references: GB:X03179; L.M.
Plant Mol. Biol. 18, 515-525, 1992
Plant Mol. Biol. 18, 515-525, 1992
A,Fitle: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A,Reference number: S20513; MUID:92163016; PMID:1371405
Nicontains: rRNA N-glycosidase (EC 3.2.2.2)
Nicontains: rRNA N-glycosidase (EC 3.2.2.2)
Signedias: Ricinus communis (castor bean)
Cipate: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
CiAccession: A24041; S20513; Ā24614; A03372; A24010; A03374; S10903
FHallingy, K.C.; Halling, A.C.; Murray, B.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A)Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
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A; Accession: S20513

A.Molecule type: DNA
A.Residues: 1-576 <TRE>
A.Residues: 1-576 <TRE>
A.Residues: 1-576 <TRE>
A.Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
R.Jumb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biocham. 148, 265-270, 1985
A.Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A.Reference number: A24614; MUID:85179479; PMID:3838723

A; Accession: A24614

A; Molecule type: mRNA A; Residues: 12-75, 10', 77-550, R',552-576 <LAM> A; Cross-references: GB: X02388; NID: 921077; PIDN: CRA26230.1; PID: 921078 R; Yoshitake, S.; Funatsu, G.; Funatsu, M. R; Yoshitake, S.; Funatsu, G.; Funatsu, M. A; Ajaric: Bold: One: 42, 1267-1274, 1978 A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile characterence number: A03372

A; Accession: A03372

A Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: 0.99-109, '8', 111-269, 'D', 272-283, 'L', 285-288, 290-302 < YOS> A. Molecule this paper cites the others in the series providing experimental details for the R. Araki, T.; Funatsu, G. B. Farski, T.; Funatsu, G. A. Farski, T.; Funatsu, G. A. Molecule A. Mo

A.Accession: A24010 A.Molecule type: protein A.Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A;Title: Primary structure of Ala chain of ricin D.

A; Reference number: A03374

A;Accession: A03374 A;Molecule type: protein

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F;212/Active site: Glu #status experimental
F;212/Active site: Glu #status predicted
F;215/Active site: Arg #status predicted
F;24-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
F;336,349,360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental
F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
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C;Date: 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261 A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
B;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
A; Bille: The primary's equence of Ricinus communis agglutinin. Comparison with ricin.
A;Reference number: A24261; MUID:86059449; PMID:2999930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
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Pred. No. 1.1e-79;
0; Mismatches 0:
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97.9%; Score 955;
Best Local Similarity 95.0%; Pred. No. 1
Matches 189; Conservative 0; Mismatch
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A; Residues: 1-564 <ROB>
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rENA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian sn N;Alternate names: alpha-TCS; type I ribosome-inactivating protein c;Species: Trichosanthes Kirilowii (Mongolian snake-gourd) c;Species: Trichosanthes Kirilowii (Mongolian snake-gourd) c;Accession: UT0566; A36274; UC1093; A36273; JT0003 Rext_change 23-Mar-2001 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. A;Alte: Cloning of trichosanthin cDNA and its expression in Escherichia coli. A;Reference number: JT0566; MUID:91153657; PMID:1999291
                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 303-325, F', 327-330, TT', 332-361, D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-65, 'Comment: This protein has strong agglutinating activity and weak cytotoxicity compared C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compared C; Superfamily: ricin; RRNA N-91ycosidase homology
C; Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed; F; 1-24/Domain: signal sequence #status predicted <ACH>
F; 2-29/Oproduct: agglutinin chain A #status predicted <ACH>
F; 35-29/Domain: RNA N-91ycosidase homology <RNG>
F; 30-364/Product: agglutinin chain B #status experimental <BCH>
F; 30-364/Product: agglutinin chain B #status experimental <BCH>
F; 30-364/Product: agglutinin chain B #status experimental cache
F; 30-364/Product: agglutinin chain B #status experimental cache
F; 30-364/Product: agglutinin chain B #status predicted
F; 30-364/Product: agglutinin chain B #status predicted
F; 30-364/Product: agglutinin chain B #status predicted
F; 30-364/Product: agglutinin chain B #status predicted
F; 30-364/Product: agglutinin chain B #status predicted
F; 30-37, 343/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 30-37, 343/Binding site: Carbohydrate (Asn) (covalent) #status experimental
F; 336, 557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribx
A;Reference number: A36274; MUID:90256790; PMID:2341400
R.Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A.fitle: The complete amino acid sequence of the B-chain of the Ricinus communis agglutin
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A;Residues: 1-233,'T',235-246,'M',248-289 <CHO>
A;Cross-references: GB:JO5434; NID:g170534; PIDN:AAA34206.1; PID:g170535
R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A;Reference number: JC1093; MUID:94271613; PMID:8003348
A;Accession: JC1093
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A;Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
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7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 FQYIEGEMRTRIRYNRRSA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.94
Matches 173; Conservative
                                                                                                                                                A, Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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A;Cross-references: GB:198346
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating T;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating T;Comment: Abrin are linked by a single disulfide bond, which is essential for toxicit C;Superfamily: ricin; FRMA N-glycosidase homology cRMC;
S;Reywords: disulfide bond, duplication; glycoprotein; glycosidase; hydrolase; lectin; py F;1-251/Product: abrin-d chain B #status predicted <ACH>
F;261-528/Product: abrin-d chain B #status predicted (ACH) #status predicted F;1/Wodified site: Uprrolidone carboxylic acid (Gln) #status predicted F;1/A,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F;200,253,361,401-430/456-473/Disulfide bonds: #status predicted F;200,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;200,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                          C,Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997 C,Accession: 832431; 834408  
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993 A;Title: Primary Structure of three distinct isoabrins determined by cDNA sequencing. Cor A;Reference number: 832429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            abrin-c precursor - Indian licorice
NyContains: RNA N-glycosidase (EC 3.2.2.2)
NyContains: RNA N-glycosidase (EC 3.2.2.2)
C.Species: Abrus precatorius (Indian licorice)
C.Spacies: Abrus precatorius (Indian licorice)
C.Spacession: S1602
R.Wood, K.A., Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
Biochem. 198, 723-732, 1991
A.Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chair A.Reference number: S16022; WUID:91266957; PMID:2050149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating. The A and B chains are linked by a single disulfide bond, which is essential for toxicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 ERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRXISN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ODQVIKĖTTEGATSQSYKOFIBALRORLIGGLIHDIPVLPDPTTVEERNRYITVELSNSE 60
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A;Molecule type: DNA
A;Residues: 1-562 <WOO>
A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
C;Comment: Abrin consists of an A chain which inhibits access: EMBL:X55667; Albert Comments and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits access and A chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a chain which inhibits a ch
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43.9%; Pred. No. 3.6e-22;
iive 22; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,171-320,'L',322-528 <HU2>
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R, Hung C.; Lee, M.; Lee, T.; Lin, J.
Bubmitted to the EMBL Data Library, March 1993
A, Reference number: S34408
                                        precatorius (Indian licorice)
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                                  Species: Abrus
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A; Molecule type: DNA
A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A; Cross-references: GB: S70176; NID: 9547148; PIDN: AAB31048.1; PID: 95547149
B; Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan J. Biol. Chem. 265, 8665-8669, 1990
A; Biol. Chem. 265, 8665-8669, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abz A; Reference number: A36273; MUID: 90256789; PMID: 2341399
                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A36273
A; Molecule type: protein
A; Residues: 24-270 cCoLs
R; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
B; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
B; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, B.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
A; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, Hua Fen (THF): history, chemistry and application
A; Reference number: J70003
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A;Reference number: A66711; PDB:11CS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
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Nat. Struct. Biol. 1, 695-700, 1994

A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A;Reference number: A58622; MUID:95360714; PMID:7634073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL'
A;Experimental source: tuber
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A;Reference number: A67092; PDB:IMRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 VSFRLSGATSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSORYALIHLTNYADE 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Huāng, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y. submitted to the Brookhaven Protein Data Bank, July 1994 A;Reference number: A67091; PDB:1MRJ
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Best Local Similarity
Matches 72; Conserv
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C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
S;35-286_Product: abrin-c chain A #status predicted <ACH>
F;41-280/Domain: rRNA N-glycosidase homology <ANG>
F;41-280/Domain: rRNA N-glycosidase homology <ANG>
F;295-562/Product: abrin-c chain B #status predicted <BCH>
F;317-359,350-400,403-441,448-483,487-256,529-562/Region: 40-residue repeats
F;317-359,350-400,403-441,448-483,487-256,529-562/Region: 40-residue repeats
F;318,Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;108,147,229,230/Bainding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;384,355,435,436/Bainding site: carbohydrate (Asn) (covalent) #status predicted
F;281-303,303-380,363-380,451-464,490-507/Disulfide bonds: #status predicted
F;322,346/Bainding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;534,555/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: Uro939; PS0163
R;Toyokawa, S.; Takeda, T.; Katc, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: Ur0393; MUID:92005921; PMID:1914000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 QDQVIKFTTEGATSQSYKQFIEALRQRLTGGLIHDIPVLPDPTTVEERNKYITVELSNSE 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 327.5; DB 2
43.9%; Pred. No. 3.9e-22;
tive 22; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82; Conservative
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A, Molecule type: protein
A, Residues: 1-247 <TOY>
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A,Status: preliminary
A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: Drotein
A,Rolecule type: Drotein
C,Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytiv
C,Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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N;Contains: karasurin A
C;Species: Trichosanthes kirilowii var. japonica
S;Species: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
C;Accession: JC5606; JC5033
C;Accession: JC5606; JC5033
B;Mizukami, H; Iida, K; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote: A;Reference number: JC5606; MUID:97356562; PMID:9212998
                                                                                                                                                                                        Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka:
A;Reference number: JC5032; MUID:97108848; PMID:8951169
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C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti:
C;Comment: This protein is a ribosome-inactivating proteins which catalytic
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;22-270/Product: karasurin C #status predicted <MAC>
F;24-270/Product: karasurin A #status predicted <MAA>
F;24-270/Product: rarasurin A #status predicted <MAA>
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Blol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka: A;Reference number: JC5032; MUID:97108848; PMID:8951169
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                         C;Species: Trichosanthes Kirilowii var. japonica
C;Dates 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C;Accession: JCS032
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
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33.4%; Score 326; DB 2;
Best Local Similarity 39.6%; Pred. No. 2.3e-22;
Matches 72; Conservative 44; Mismatches 50;
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Trichosanthes kirilowii
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Best Local Similarity
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A;Molecule type: protein
A;Residues: 22-270 <KON>
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A;Residues: 1-289 <MIZ>
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Abrin-a precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Species: Abrus precatorius (Indian licorice)
C;Accession: S3429; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
A;Hung, C.H. Biol. 229, 263-267, 1993
A;Tile: Frimary structure of three distinct isoabrins determined by cDNA sequencing. Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: C39761; S14471
R;Evensen, G.; Mathiesen, A.; Sundan, A.
J:Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
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C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin
C;R-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology *CPT-246/Domain: rRNA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 EVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 INFTIAGATVOSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 61
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A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295.
A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295.
A;Note: the coding region for the sequence shown is preceded by an ATG codon A;Note: residues 1-8 were derived from the synthesized primer
R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 'M',1-251 <EV2>
A;Cross-references: EMBL:X54872; NID:g16089; PIDN:CAA38654.1; PID:g16089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-251 <RVB>
R;Evensen, G; Mathlesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                   abrin (clone 7.2) precursor - Indian licorice (fragment) N;Contains: rRNA N-glycosidase (EC 3.2.2.22) C;Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Reference number: S32429; MUID:93132798; PMID:8421313
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A;Status: nucleic acid sequence not shown
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173 RVGVSIRTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Reference number: S14471
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nes 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S14471
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Matches
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A; Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-430
A; Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-430
C; Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-430
C; Residues: abroaches seed
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Reywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; procession abroaches benain A #status predicted acts.
F; 1250-1270 Product: abrin-b chain B #status experimental <BCH>
F; 260-527 Product: abrin-b chain B #status experimental <BCH>
F; 260-527 Product: abrin-b chain B #status appendicted
F; 140-1359 Associated (300 Associated (300 Associated) Associated
F; 140-1359 Associated (300 Associated) Associated
F; 140, 360, 400 (Binding site: carbohydrate (300 (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (300) (
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C.Species: Abrus precatorius (Indian licorice)
C.Species: Abrus precatorius (Indian licorice)
C.Accession: 832430; UC1399
R.Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
A.Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by CDNA sequencing. CC
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Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxid
A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                                                                                                                                                                                                          85 VAIDVINVYVMGYRAGDISYFF---NEASAIEAAKYVFKDAKRKVTLPYSGNYERLQIAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 ELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYDRL 117
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                                                                                                                                                                                                                                                        63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                        INFITAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                       ----VLPNRVGLPINQRFILVELSNHA 57
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Best Local Similarity
Matches 83; Conserva
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RV 198
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F;5-246/Domain: rRNA N-glycosidase homology <RNG>
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                                              10 INFTTAGATVQSYTNFIRAVRGRL-
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A,Rolecule type: procein
A,Rolecule type: procein
A,Rolecule type: procein
A,Rolecule type: procein
A,Rolecule type: procein
A,Rolecule type: procein
A,Rolecule source: seed
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh taining receptors on the cell surface. The A and B chains are linked by a single disulfic C;Superfamily: ricin; rRNA N-glycosidase homology
C,Reywords: duplication; glyCoproceinin; glycosidase; hydrolase; lectin; pyroglutamic acid
F;1-251/Product: abrin-a chain A #status experimental <a href="#">ACH></a>
F;246/Domain: rRNA N-glycosidase homology <a href="#">RNA</a>
F;246/Domain: rRNA N-glycosidase homology <a href="#">RNA</a>
F;288-325,326-366,369-407,414-449,455-528/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;74,113,195,196/Binding site: Glu, ARN # #status predicted
F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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A;Cross-references: GB:X54872
A;Cross-references: GB:X54872
A;Note: residues: 1-8 were derived from the synthesized primer
A;Note: residues: 1-8 were derived from the synthesized primer
B;Simura, M; Sumizawa, T; Funatsu, G.
B;Simura, M; Sumizawa, T; Funatsu, G.
B;Simura, M; Sumizawa, T; Funatsu, G.
B;Simura, M; Sumizawa, T; Funatsu, G.
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxid
A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Residues: 261-347, T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 «KIM»
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 
                                         frd
                                                                                                                                                             A Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: Leaning the forms pyrrolidone carboxylic acid; therefore, we have
B. Molec: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
B. Brol. Chem. 266, 6848-6852, 1991
A. Hitle: Direct molecular cloning and expression of two distinct abrin A-chains.
A. Reference number: A39761; MUID:91201329; PMID:2016300
A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein A;Reference number: J70202
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Molecule type: protein
A, Rolling S. H.; Chow, L. P.; Chen, Y. L.; Liaw, Y. C.; Chen, J. K.; Lin, J. X.
R, Lin, S. H.; Chow, L. P.; Chen, Y. L.; Liaw, Y. C.; Chen, J. K.; Lin, J. X.
R, Lin, S. H.; Chow, L. P.; Chen, Y. L.; Liaw, Y. C.; Chen, J. K.; Lin, J. X.
R, Lin, S. Biochem. 240, 564-569, 1996
A, Title: Probing the domain structure of abrin-a by tryptic digestion.
A, Reference number: S74110; MUID:97008945; PMID:8856055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'ME', 2-251 <EV2>
A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
R;Chen, Y.L.; Chow, L.P.; Tsugita. A: Lin T v
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41.1%; Pred. No. 5.7e-20;
iive 26; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: A39761
A,Status: mucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 'E',2-251 <EVE>
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A,Molecule type: protein
A,Residues: 89-108,154-172 <LIN>
A,Experimental source: seed
A,Accession: S74111
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                                                                          A;Reference number: JT0202
A;Accession: JT0202
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beta-luffin - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Accession: 823519; 823113
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
R;Kataoka, J.; Habuka, N.; Miller, Masuta, C.; Koiwai, A.
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
A;Reference number: 823519; MUID:92353400; PMID:1643290
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                                                                                                                                                                                                    65 EVGIDVTNAYVAYRAĞTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                                                   120 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGEM 179
                                                                                                                                                                                                                                                                                                                         119 WAHQSRQOIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                         62 TLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ
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----TVLPNRVGLPINQRFILVELSNHAELSV
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A;Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology «RNG»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 300.5; DB 2; 35.3%; Pred. No. 4.7e-20; ative 43; Mismatches 57;
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Length 250;

DB 2;

30.1%; Score 293.5;

Query Match

Best Local Similarity   33.7%;   Pred. No. 1.88-19;   Matches   63;   Conservative   46;   Mismatches   57;   Indels   21;   Gaps   4;	OY 10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN
172 IERIPKN 178  SULT 14 2494  NA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loofah Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A Species: Luffa cylindrica (smooth loofah) Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999 Accession: S2494; S26399; #J0202; A32542 Accession: 2,7 Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A. ant Mol. Biol. 18, 1199-1202, 1992	REBULT 15 RLPUGG rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor [validated] - balsam pear N-blternate names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin alpl C;Species: Momordica charantia (balsam pear, bitter gourd) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 15-Sep-2000 C;Accession: S14273; A61318; S16490; UN0628; S01670 R;HO, W.K.X.; Liu, S.C.; Shaw, P.C.; Yeungy H.W.; Ng, T.B.; Chan, W.Y. Biochim. Biophys. Acta 1088, 311-314, 1991 A;Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein. A;Reference number: S14273; MUID:91159486; PMID:2001404
tivating prot protein from	A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-286 < HOW> A; Cross-references: EMBL.X57682; NID:g19527; PIDN:CAA40869.1; PID:g19528 A; Cross-references: EMBL.X57682; NID:g19527; PIDN:CAA40869.1; PID:g19528 B; Li, S.S.L. B; R; Li, S.S.L. A; Title: Purification and partial characterization of two lectins from Momordica charant; A; Reference number: A61318; MUID:80201763; PMID:7379938 A; Reference number: A61318 A; Residues: 24-50 < LIA> A; Residues: 24-50 < LIA> A; Residues: 24-50 < LIA> A; Note: as a lectin shows agglutinating activity for type-O red blood cells A; Monte: of some ribosome-inactivating proteins. B; Monte cucchi, P. C.; Lazzarini, A. M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D. Int. J. Pept. Protein Res. 33, 263-267, 1989 A; Title: N-terminal sequence of some ribosome-inactivating proteins. A; Reference number: S1631: MITD:8432641; PMID:2575496
Fitle: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from deference number: JH0202, MUID:91197482; PMID:1368623 Accession: JH0202 Accession: JH020	A,Accession: \$16490 A,Rolecule type: protein A,Rolecule type: protein A,Rolecule type: protein B; Minami, Y.; Funatsu, G. B; Minami, Y.; Funatsu, G. B; Minami, Y.; Funatsu, G. B; Mitle: The complete amino acid sequence of momordin-a, a ribosome-inactivating protein A,Fitle: The complete amino acid sequence of momordin-a, a ribosome-inactivating protein A,Feference number: UN0628, MUID: 93372485; PMID: 7763984 A,Roccession: UN0628 A,Rolecule type: protein A,Residues: 24-107, Q',109-123,125-147, L',149-154,'I',156-205,'I',207-208,'L',210-214,'I A,Experimental source: seed R,Fen, J; Mang, Y; Stuart, D.I. S; Mong, Y; Stuart, D.I. S; Short Mang, Y; Dong, Y; Stuart, D.I. S; Short Mang, Y; Dong, N; Stuart, D.I.
A.Residues: 21-28,'G',30,'X',32-34,'K',36-40 <ram> C.Function: A.Description: Yordolyzes the N-glycosidic bond of a specific adenosine in 285 rRNA ther C.Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology C.Keywords: glycoptotein; glycosidase; predicted <sig> F.20-Domain: signal sequence #status predicted <sig> F.21-26/Domain: signal sequence #status predicted <sig> F.22-26/Domain: rRNA N-glycosidase alpha-luffin #status experimental <mat> F.26-20/Domain: rRNA N-glycosidase homology <rng> F.26-27/Domain: rRNA N-glycosidase homology <rng> F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-26-27/Domain: rRNA N-glycosidase homology cRNG&gt; F.26-26-27/F.COM</rng></rng></mat></sig></sig></sig></ram>	A,Reference number: A52272; PDB:1AHC A,Robtents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-269 B,Rubsain, J.; Tickle, I.J.; Wood, S.P. submitted to the Brockhaven Protein Data Bank, March 1994 A,Reference number: A52385; PDB:1MOM A,Reference number: A52385; PDB:1MOM A,Reference number: A52385; PDB:1MOM A,Reference number: A67089; PDB:1MOM A,Reference number: A67089; PDB:1MRH A,Reference number: A67089; PDB:1MRH A,Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, R',79-132,' C,Function: A,Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA there C,Superfamily: RNA N-glycosidase; rRNA N-glycosidase homology C; Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin F;1-18/Domain: signal sequence #status predicted <pig>F;19-23/Domain: amino-terminal propeptide #status predicted <pig>F;19-23/Domain: amino-terminal propeptide #status predicted <pig< td=""></pig<></pig></pig>

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F;24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>
F;27-266/Domain: carboxyl-terminal propertide #status predicted <CTP>
F;270-286/Domain: carboxyl-terminal propertide #status predicted <CTP>
F;93,183,186/Active site: Tyr, Glu, Arg #status predicted
F;95,0/Binding site: carbohydrate (Asn) (covalent) #status experimental
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	4;	62	84
	Gaps	AELSVI	DGKTIT
	16;	ELSNH	HLFNY)
ength 286	Indels	NORFILV	:   : /SGAGRYLLM
Query Match 28.0%; Score 273; DB 1; Length 286; Rest Local Similarity 34 8%; Dred No. 1 6e-17.	Matches 63; Conservative 40; Mismatches 62; Indels 16; Gaps 4;	10 INPITAGATVOSYINFIRAVRGRLIVLPNRVGLPINORFILVELSNHAELSVI 62	KDLRNALPFREKVYNIPLLLPS
28.0%	Conservative	INFTTAGATVOSYTNEI	SFRLSGADPRSYGMFI
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63 LALDVINAYVVGYRAGNSAYFFHPDNQEDAB-ALTHLFTDVQNRYTFAFGGNYRLEQLA 121
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<sup>182</sup> R 182

<sup>197</sup> R 197

Search completed: February 10, 2004, 16:28:04 Job time: 11.2817 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:13:55; Search time 6.33803 Seconds (without alignments) 1409.756 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-083-336A-11 975 1 MIFPKQYPIINFTTAGATVQ......RFQXIBGEMRTRIRYNRRSA 190

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		c	ricinus com		trichosanth	abrus preca	trichoganth	us preca	bryonia dio	sambucus ni	ω. O	us preca	fa cylin	umis fig	luffa cylin	momordica c	momordica b	viscum albu	trichosanth	gelonium mu	phytolacca	mirabilis j	phytolacca	phytolacca	saponaria o	saponaria o	phytolacca	saponaria o	saponaria o	dianthus ca	hordeum vul	saponaria o	bacteriopha	hordeum vul	таув (т
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SUMMARIES		QI	RICI RICCO	AGGL_RICCO	RIPT TRIKI	ABRC_ABRPR	RIPS_TRIKI	ABRB ABRPR		NIGB SAMNI	RIP1_BRYDI	ABRA ABRPR		RIP1 CUCFI	RIPA_LUFCY	RIP1 MOMCH	RIP2_MOMBA	MLA VISAL	RIPI_TRIAN	RIPG_GELMU	RIPA PHYAM		RIP1_PHYAM	RIPS_PHYAM		RIP5_SAPOF		RIP6_SAPOF		RIPO_DIACA			SLTA_BP933		RIP3_MAIZE
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RIPX MAIZE RIP9_MAIZE SLYA_BBH19 SLYA_BBH19 SYV_ĀQUAE JIGO_DORVU Y348 MYCRN ORPB_HUMAN HART_YBCH RIP4_SAROF NPRV_VIBPR GPH_HAETN
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## ALIGNMENTS

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MEDLINE=93165632; PubMed=1287657;

A Kin Y., Robertus J.D.;

A Kin Y., Robertus J.D.;

A Kin Y., Robertus J.D.;

"Analysis of several key active site residues of ricin A chain by

"Analysis of several key active site residues of ricin A chain by

"Analysis of several key active site residues of ricin A chain by

"The content of the content content is responsible for inhibiting to protein synthesis through the catalytic inactivation of 608 ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 288 ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the for cell agglutination (Lectin activity). It binds to beta-D-

C -1-GATALYTC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific adenosine on the 28S frna.
SUBUNIT: Disulfide-linked dimer of A and B chains.
DOMAIN: The B chain is composed of two domains, each domain osnists of 3 homologous subdomains (alpha, beta, gamma).
PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
                                                                                MEDLINE=87165983; PubMed=3558397; Mondingo A.F., Ernst S.R., Katzin B., Monfort W., Villafranca J.E., Mondingo A.F., Ernst S.R., Katzin B., Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.; "The three-dimensional structure of ricin at 2.8 A."; J. Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
MEDLINE=96374222; PubMed=8780513;
Day P.J., Ernst S., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svinth M.C., Robertus J.D.;
"Structure and activity of an active site substitution of ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure-based identification of a ricin inhibitor.";
J. Mol. Biol. 266:1043-1049(1997).
[14]
                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDLINE=91352005; PubMed=1881882; Rutenber E., Robertus J.D.; "Structure of ricin B-chain at 2.5-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
MEDLINE=95082010; PubMed=7990130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN
                                                                                                                                                                                                                                       MEDLINE=91352004; PubMed=1881881;
Katzin B.J., Collins E.J., Robertus J.D.;
"Structure of ricin A-chain at 2.5 A.";
Proceins 10:251-259(1991).
                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lochemistry 35:11098-11103(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. 244:410-422(1994).
                    Toxicon 39:1723-1728(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins 10:260-269(1991).
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  "Ricin."
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
-!- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
-!- DATABASE: NAME=Protein Spotlight;
NOTE=Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN, 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | N-LINKED (GLCNAC. ..). | FIIda-CAR 000080. | N-LINKED (GLCNAC. ..) (IN MINOR FORM). | FIIda-CAR 000081. | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ..). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). | N-LINKED (GLCNAC. ...). 
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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-> R (IN REF. 3).
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LINKER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN
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PDB; 1114; 16-JAN-02.
PDB; 1114; 16-JAN-02.
PDB; 1114; 16-JAN-02.
GlycoSuiteDB; P02879; -.
InterPro; 1PR001572; Ricin B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00052; Ricin B_lectin, 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
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2-ALPHA.
2-BETA.
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EMBL, X52908; CAA37095.1; -.
EMBL, X02388; CAA26230.1; -.
EMBL, A12892; CAA01058.1; -.
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353
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1APG; 31-JAN-94.
1FMP; 31-OCT-93.
1IFS; 14-JAN-98.
1IFT; 14-JAN-98.
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1BR6;
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                                                                                                                                                                               52 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                  GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                            36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
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MEDLINE=80178723; PubMed=6768555;
Lin T.T.-S., Li S.S.-L.;

Lin T.T.-S., Li S.S.-L.;

"Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";

Eur. J. Biochem. 105:453-459(1980).

-! - CATALYITY CACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the SES FRNA.

-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86059449; PubMed=2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with
                                                                               ---VLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
NCBI_TaxID=3988;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Araki T., Yoshioka Y., Funatsu G.; The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (BC 3.2.2.22); Agglutinin B chain].
Ricinus communis (Castor bean).
                                        10;
Score 955; DB 1; Length 576;
Pred. No. 1.5e-81;
0; Mismatches 0; Indels
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                                                                             2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                    216 FOYIEGEMRTRIRYNRRSA 234
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  97.9%;
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                                    Matches 189; Conservative
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85 ELSNHAELSVTLALDVTNAXVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG 144
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       HSSP; P02879; 1BR6.

Glycosultenb; P06750; -.

InterPro; IPR00172; Ricin_B_lectin.

Efam; PR0052; Ricin_B_lectin, 6.

Pfam; PR00356; RHIGARICIN.

SMART; SM00458; RICIN; 2.

PROSITE; PS00231; RICIN; 2.

PROSITE; PS00231; RICIN, 1.

PROSITE; PS00275; SHIGA RICIN; 1.

PROSITE; PS00275; SHIGA RICIN; 1.

PROSITE; PS00275; SHIGA RICIN; 1.

Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; dilycoprotein; Lectin; Signal.
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BY SIMILARITY.

N-LINED (GLCNAC. .) (POTENTIAL).

N-LINED (GLCNAC. .).

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N-LINED (GLCNAC. .).

F -> T (IN REF. 2).

N -> D (IN REF. 2).

R -> G (IN REF. 2).

R -> T (IN REF. 2).

R -> T (IN REF. 2).

R -> T (IN REF. 2).

R -> T (IN REF. 2).

R -> T (IN REF. 2).
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                              INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62851 MW; D455F2A72F609759 CRC64;
                                                                                                                                                                                            AGGLUTININ B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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LINKER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.8%; Score 865.5; DB 1
86.9%; Pred. No. 3.3e-73;
live 7; Mismatches 8
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PIR; A24261; RLCSAG
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PDB; 1002; 24-APR-00.
InterPro; IPR001574; RIP.
PRAM; PR00161; RIP; 1.
PRANTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; Sinxin, Signal; 3D-structure.
SIGNAL 24 270 RIBOSOME-INACTIVATING PROTEIN ALPHA-

TRICHOSANTHIN.
MISSING IN MATURE PROTEIN.
BY SIMILARITY.
IPLL -> LPLI (IN REF. 4).
MISSING (IN REF. 4).

ACT SITE CONFLICT CONFLICT

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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-!- TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Maximowicz; TISSUE=Leaf;
MEDLINE=90256790; PubMed=2341400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-linactivating protein.";
J. Biol. Chem. 265:8670-8674 (1990).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Sperimatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Trichosanthes.
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Pure Appl. Chem. 58:789-798(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R., Wu P., Hwang K., Piatak M.;
"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
                                                                                                                                                                                                                                    MEDLINE=91153657; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=95344383; PubMed=7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
MEDLINE=94344957; PubMed=9066085;
Stou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 24-270.
STRAIN=Maximowicz; TISSUE=Tuberous root;
MEDLINE=90256789; PubMed=2341399;
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Gene 97:267-272(1991).
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V -> VDAGLPRNAVL (IN REF. 4).
KI -> GL (IN REF. 4).
K -> S (IN REF. 4).
WS -> LWL (IN REF. 4).
C -> T (IN REF. 4).
S -> T (IN REF. 2).
MISSING (IN REF. 2).
T -> M (IN REF. 2).
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Best Local Similarity 38.99
Matches 72; Conservative
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EMBL; M34858; AAA34207.1; -. EMBL; J05434; AAA34206.1; -.

PIR; JT0566; RLTZT.

IMRJ; 07-FEB-95. IMRK; 07-FEB-95. ITCS; 10-JUL-95. 1J4G; 28-JAN-03.

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WEDLINE-91266957; PubMed=2050149;
Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;
Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;
Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;
Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;

"Preproabtin: genomic clouing, characterisation and the expression of the A-chain in Escherichia coli."

"Eur. J. Biochem. 198:723-732(1991).

"Eur. J. Biochem. 198:723-732(1991).

"I. FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SOURDING ADENINE FROM POSITION 4,324 OF 28 S.RRNA. THE SCHALTYTIC ACTIVITY: Endohydrolysis of the N-91ycosidic bond at one specific adenosine on the 28S FRNA.

"I. CATALYTIC ACTIVITY: Endohydrolysis of the N-91ycosidic bond at one specific adenosine on the 28S FRNA.

"I. DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

"I. DOMAIN: THE B CHAIN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY: TYPE 2 RIP SUBFAMILY:

"I. TILL J. SIMILARITY: CONTAINS 2 FIGH B CHAIN GONDAINS."

"I. TYPE 2 RIP SUBFAMILY: CONTAINS 2 FIGH Decin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                        82 TISVAIDVINVXIMGYRAGDISYFF---NEASAIEAAKYVFKDAMRKVILPYSGNYERLQ 138
                                                                                                                                                                                                                          60 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-BAITHLFTDVQNRYTFAFGGNYDRLE 118
                                                                                                                                                                                         119 QIAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                              ::| :|| || || :|:|:|
25 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 81
INFITAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor; (Rel. 41, Last annotation update)
Abrin-c precursor; Abrin-c B chain)
(EC 3.2.22); Abrin-c B chain)
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; endicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae, Abrus.
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PROSITE; PS50231; RICIN B LECTIN, 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
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InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin B lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                   194 IGKRV 198
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P28590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ERWAHQTREEISLGLQALTHAIS---FLRSGASNDEBKARTLIVIIQMASEAARXRYISN 207
                                                                                                                                                                                                                                                                                                                                                                                              6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizukami H., Iida K., Kondo T., Ogihara Y.; "Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes kitilowii var. japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                             35 QDQVIXFTTEGATSQSYKQFIEALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Rosidae,
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                     15; Gaps
                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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         BY SIMILARITY.

ABRIN C A CHAIN (BY SIMILARITY).

LINKER PEPTIDE (BY SIMILARITY).

ABRIN C B CHAIN (BY SIMILARITY).

RICIN B-TYPE LECTIN 1.

RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                          33.6%; Score 327.5; DB 1; Length 562; 43.9%; Pred. No. 5.3e-23;
                                                                                                                                                                BY SIMILARITY.
INTERCRIAIN (BY SIMILARITY).
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BY SIMILARITY.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
 Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                     68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.22)
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                         62817 MW; IFDOABC7D7BA6278 CRC64;
                                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                    22; Mismatches
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N-LINKED
                                                                                                                              2-ALPHA.
2-BETA.
2-GAMMA.
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1-GAMMA.
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                                                                                         L-ALPHA.
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Biol. Pharm. Bull. 20:711-713(1997).
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MEDLINE-97356562; PubMed-9212998;
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MEDLINE=92005921; PubMed=1914000;
Signal;
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395
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 Glycoprotein; Lectin;
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395 3
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562 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                 -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abril Barkk Standaku; PRT; 527 AA.

206077; P81374;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 31, Last sequence update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(BC 3.2.2.2.7; Abrin-b B chain)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Gaps
                                                                                                              specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                Chem. Pharm. Bull. 39:1244-1249(1991).
-!- FUNCTION: ABORTION-INDUCING PROTRIN. IT INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
                                                                                                                                                                                                                                                                                                                              PIR; JC5606; JC5606.
PIR; JU0393; JU0393.
HSSP; P09989; JMMJ.
InterPro; JPR001574; RIP.
PRINTS; PR00396; SHIGARICIN.
PROUNTS; PS00275; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
PROSITE; Signal.
TOWN: Signal.
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.4%; Score 326; DB 1; Length 289; 39.6%; Pred. No. 3.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KARASURIN-A.
REMOVED IN MATURE FORM.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KARASURIN-C.
                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                         EMBL; AB000666; BAA21786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31704 MW;
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les 72; Conservative
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270
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289
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183 1
289 AA;
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                                karasurin."
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                                                                                                                                                                                                                                                                                                          PRECEDES ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one apecific adenosine on the 28S rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-PERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFRAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS05231; RICIN B LECTIN; 2.
PROSITE; PS05275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Pyrrolidone carboxylic acid.

CHAIN

ABRIN-B A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                         Kimura M., Sumizawa T., Funatsu G.,
"The complete amino acid sequences of the B-chains of abrin-a and
abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biosci. Biotechnol. Biochem. 57:166-169(1993).

1- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL
SUBMINTS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
ABRIN-A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
               Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
Pyrhary structure of three distinct isoabrins determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABRIN-B B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKER PEPTIDE
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1-GAMMA.
2-ALPHA.
2-BETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S32430; S32430.
HSSP; P11140; IABR.
InterPro; IPR000772; Ricin B lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin B lectin; 6.
Pfam; PF00161; RIP; 1.
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MEDLINE=93132798; PubMed=8421313;
                                                                                                                               MEDLINE=93169023; PubMed=7763422;
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                                                                                                SEQUENCE OF 260-527.
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DISULFID
DISULFID
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CARBOHYD
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61 TESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYIDL 116
                                                                                                                                                                                                                                                                                               58 ELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                               118 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                             6 QYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSNHA
                                                                                                                                                                                                                     Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Siegall C.B., Gawlak S.L., Marquardt H.,
"Bryodin 2 a ribosome-inactivating protein isolated from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioconj. Čněm. 5:423-429(1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of ribosome-inactivating proteins isolated Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                            DB 1; Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P98184; Q9S8JO,
16-OCT-2010 (Rel. 40, Created)
16-OCT-2010 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA N-glycomidase) (RC 3.2.2.22) (BD2).
                                                                                                                                                                                                                     69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.
                                                                                                                                                                   3253AE490CE9494A CRC64;
                                                                                                                                                                                                         1.3e-22;
                                                 Y -> D (IN REF. 2
N -> S (IN REF. 2
N -> S (IN REF. 2
H -> Y (IN REF. 2
R -> G (IN REF. 2
R -> G (IN REF. 2
H -> W (IN REF. 2
H -> Y (IN REF. 2
H -> Y (IN REF. 2
                                                                                                                                                                                                                     21; Mismatches
                         S -> N (IN E
                                                                                                                                                                                            33.1%; Score 323;
                                                                                                                                                                                                          Pred. No.
 N ^-
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                                                                                                                                                                     59114 MW;
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                                                                                                                                                                                                                     83; Conservative
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 291
3351
3351
3426
4428
4431
4491
5002
513
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                                                                                                                                                                  527 AA;
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 2291
3350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 TVALDVVNVYVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLETAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 INFTTAGATVQSYTNFIRAVRGRLTV-LPNRVGLPINQ-----RFILVELSNHAELSV 61
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                                                                                                                                                                                                                                                                                                                                 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 İNFSLIGATGATYKTFIRNLRITKITVGTPRVYDIPVLRNAAAGLARFQLVTLTNYNGESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIGB_SAMNI STANDARD; PRT; 563 AA.
P33183; P33184; P93542;
01-0CT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Nigrin b precursor (Agglutinin V) (SNAV) (Concains: Nigrin b A chain FIRA N-9Jycosidase) (EC 3.2.2.22); Nigrin b B chain)
Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94003077; PubMed=8400135;
Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
Munoz R., Arias F.J., Calonge M., Gazcia J.R., Mendez E.;
"Isolation and partial characterization of nigrin b, a non-toxic
novel type 2 ribosome-inactivating protein from the bark of Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 22:1181-1186(1993).
-!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                      .) (POTENTIAL).
                                                                                                                                                                                                                                                 PROSITE, PS00275, SHIGA RICIN, 1.
Plant defense, Protein Synthesis inhibitor; Hydrolase, Toxin;
Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                          C52BE2F6A873769C CRC64;
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le-22;
- 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 320.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                 EMBL; I34238; -; NOT_ANNOTATED_CDS. HSSP; P09989; 1MRJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bark;
MEDLINE=96215449; PubMed=8647092;
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25 25 N
282 AA; 30754 MW;
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                                                                                                                                                                                          InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
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                                                                                                                                                                                                                                                                                                                               282
183
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PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM FOSITION 4,324 OF 28 S. RRNA. THE B. CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                             CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS0231; RICIN B_LECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Glycoprotein; Lectin; Signal.
                                                                                                          epecific adenosine on the 285 rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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(POTENTIAL).
(POTENTIAL).
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INTERCHAIN (BY SIMILARITY)
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F250CBE24621BF14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIGRIN B A CHAIN.
NIGRIN B B GLAIN.
RICIN B-TYPE LECTIN 1.
1-ALPHA.
1-BETA.
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2-GAMMA.
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563 AA;
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                                  P31185; 095819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(RC 3.2.2.2) (BBI)
Bryonia dioica (Red bryony)
Bryonia dioica (Red bryony)
Bryonia dioica (Red bryony)
Shkaryota, Viridiplantae, Streptophyta; Enbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae, Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ANTICOL IN ANTICOL CELLO.

-1- CATALYTIC ACTORNATION CELLO.

-1- CATALYTIC Adenosine on the 28S FRNA.

-1- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO
                                                                                                                                                                                                                                                                                                                                                                                             "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                MEDLINE=97228081; PubMed=9115985;
Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOCODI, Chem. 5:423-429 (1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N"-terminal sequence of some ribosome-inactivating proteins."; Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
                       290 AA
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                       PRT;
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                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 31.5%; Score 307.5; DB 1 Similarity 38.4%; Pred. No. 3.9e-21; 73; Conservative 36; Mismatches 56
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                                                             RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN. BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
E-XF. REDUCES ACTIVITY 10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                             Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; 3D-structure; Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                        DB 1; Length 290;
                                                                                                                                                                                                                                                                                                                             31738 MW; E966CD9C031A42DB CRC64;
                                                                                                                                                                                                                                                                                                                                       31.3%; Score 305; DB 1.35.7%; Pred. No. 3e-21;
send an email to license@isb-sib.ch)
         EMBL; 124020; -; NOT_ANNOTATED_CDS. PTR; S16491; S16491. PDB; BRY; 04-WAR-9. InterPro; IPR001574; RIP.
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Best Local Similarity
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63 LALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121

10 INFITAGATVOSYTNFIRAVRGRLTVLPNRVGLPI-----NORFILVELSNHAELSVT 62 

84

Gaps

16;

56; Indels

45; Mismatches

Conservative

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122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECEDES ENDOCYTOSIS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CEMIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                       P11140; P28589;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 29, Last sequence update)
28-FE2-2003 (Rel. 41, Last annotation update)
Abrin-a precursor (Contains: Abrin-a A chain (rRNA N-glycosidase)
(RC 3.2.2.2); Abrin-a B chain].
(RC 3.2.2.2); Abrin-a Strain-a Carb's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-251.
TISSUE-Seed;
Funatus G., Taguchi Y., Kamenosono M., Yanaka M.;
Funatus G., Taguchi Y., Kamenosono M., Yanaka M.;
The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **CRAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).

**MEDLINE=9533188; PubMed=5608980;

Tabliov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;

"Crystal structure of abrin-a at 2.14 A.";

J. Mol. Biol. 256:354-367(1995).

-- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBINITYS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. ABRIN A IS MORE TOXIC THAN RICIN.

--- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITY THE STRUCK ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=93132798; PubMed=8421313;

Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDLINE=92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
FEBS Lett. 309:115-118(1992).
                                                                                                                                                                                                                                                                               528 AA.
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                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                     182 RI 183
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INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

--- SIMILARITY: Contains 2 ricin B-type lectin domains.

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Gaps

Length 528; Indels 19;

INFITAGATVOSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 61

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RESULT 13
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                                                                                             119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
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                                                          TLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 119
                                                                                                                                                          120 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Luffa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91248488; PubMed=1368666;
Islam M.R., Hirayama H., Funatsu G.;
"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gound (luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-238(1991).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
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PROSITE; PS00275; SHIGA RICIN, 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific adenosine on the 28S rRNA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             176 RVSIQ 180
                                                                                                                                                                                                                                                               180 RTRIR 184
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada T., Ohki S.T., Osaki T.;
"Cloning and analysis of a cDNA coding a putative ribosome-
"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";
Plant Biotechnol. 17:337-340 (2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28s rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
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                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
(EC 3.2.2.22).
                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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Pfam; PR00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGAR RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
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286 PUTATIVE RIBOSOME-INACTIVATII
185 BY SIMILARITY.
103 N-LINKED (GLCNAC. . .) (POTE:
110 N-LINKED (GLCNAC. . .) (POTE:
252 N-LINKED (GLCNAC. . .) (POTE:
A; 31771 MW; 4EFD4966E604DA41 CRC64;
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HSSP; P16094; 1AHC.
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Conservative 4
                                                               STANDARD;
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252
286 AA;
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hes 60; Conserv
                                                                                                                                                                                                                                                                                                                                                               eurosida I; Cucurb
NCBI TaxID=131071;
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SEQUENCE
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RESULT 12
RIP1_CUCFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 KAITVAVDVINVYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYEKLQ 134
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                                                                                                                                                                                                                                                                                                                                                          -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
--- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
--- TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 INFITAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN-------QRFILVELSNHAE
                                                                                                                                                               core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Gaps
                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.2)
Luffa cylindrica (Smooth Loofah) (Sponge gourd).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Rosidieurosids I; Cucurbitales; Cucurbitaceae; Luffa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
Toxin; Signal.
                                                                                                                                                                                                                                                                   MEDLINE=92268316; PubMed=1600156;
Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
inactivating protein from Life cylindrica.";
Plant Mol. Biol. 18:1159-1202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.2%; Score 274.5; DB 1; Length 277; 33.3%; Pred. No. 2e-18;
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 277 AA.
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BY SIMILARITY.
PRT;
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InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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 STANDARD;
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RESULT 14

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Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S. Tang Y., Jin S., Wang Y.;
"Studies on crystal Structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298(1995).
-!- CATALIVIIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
               01-APR.1990 (Rel. 14, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
15-SEP-2003 (Rel. 42, Last amnotation update)
Ribosome-inactivating protein momordin I precursor (rRNA N-glycosidase) (EC 3.2.2.2) (Alpha-momorcharin) (Alpha-MMC).
Noglycosidase) (EC 3.2.2.2) (Alpha-momorcharin) (Alpha-MMC).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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-I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
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MEDITNE=91159486; PubMed=2001404;
HO W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;
"Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casellas P., Dussossoy D., Falasca A.I., Barbieri L., Guillemet J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F., "Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii Maximowicz. Purification, partial characterization and use for preparation of immunotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94356447; PubMed=8075985; Ren J., Mang Y., Dong Y., Stuart D.I.; "The N-qlycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of alpha-momorcharin."; Structure 2:7-16(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N'terminal sequence of some ribosome-inactivating proteins.";
Int. J. Pept. Protein Res. 33:263-267(1989).
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Husain J., Tickle I.J., Wood S.P.,
"Crystal structure of momordin, a type I ribosome
protein from the seeds of Momordica charantia.";
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Eur. J. Biochem. 176:581-588(1988).
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MEDLINE=89005108; PubMed=3262509;
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P16094; P24697;
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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286 AA; 32031 MW;
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PDB; 1CF5; 07-JUN-99.
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InterPro; IPR001574; RIP.
Pfam, PF00161; RIP.
PFUNTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
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142 GKPREXIPIGLPALDSAISTLIHYDS----TAAAGALLVLIQTTAEAARFKYIEQQIQE 196
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"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologous to other plant proteins.";
Nucleic Acids Res. 20:4662-4662(1992).
I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-: SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
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01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momoratin Iprecursor (rRNA N-glycosidase) (BC 3.2.2.2)
Nomoratica balsamina (Bitter gound) (Balsam pear).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae; eurosids 1; Cucurbitales; Cucurbitaceae; Momoratica.
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3B89FF1AE6B25986 CRC64;
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141 KIRENIDLGLPALSSAITTLFYYNA-----QSAPSALLVLIQTTAEAARFKYIERHVAKY 195 g

183 IRYN 186

à qq

: 196 VATN 199

Search completed: February 10, 2004, 16:23:26 Job time : 6.33803 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:17:00 ; Search time 25.3521 Seconds (without alignments) 1933.961 Million cell updates/sec Run on:

US-10-083-336A-11

Perfect score:

1 MIFPKQYPIINFTTAGATVQ......RFQYIEGEMRTRIRYNRRSA 190 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 Total number of hits satisfying chosen parameters:

830525 segs, 258052604 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database :

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp archa: \*
sp bacteria: \*
sp fung: \*
sp fung: \*
sp human: \*
sp mammal: \*
sp mammal: \*
sp phage: \*
sp phage: \*
sp phage: \*
sp phage: \* sp\_bacteriap:\* sp\_archeap:\* rvirus:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q41174 ricinus com	Q94bw3 cinnamomum	Q94bw4 cinnamomum	Q94bw5 cinnamomum	Q9fv22 cinnamomum	Q94ke4 trichosanth	Q41216 trichosanth	004367 sambucus ni	Q9lre3 trichosanth	Q9avr2 sambucus eb	Q06076 abrus preca	Q8lpv7 trichosanth	Q38760 abrus preca	Q945s2 sambucus ni	Q8gt32 sambucus ni	Q41611 trichosanth
SUMMARIES			ID	041174	Q94BW3	Q94BW4	Q94BW5	Q9FV22	Q94KE4	041216	004367	Q9LRE3	Q9AVR2	920900	Q8LPV7	Q38760	094552	Q8GT32	041611
			- 1	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
			Match Length DB	541	280	580	581	549	289	289	563	247	564	528	270	252	563	563	270
	₩	Query	Match	97.9	38.4	38.2	38.0	37.8	34.3	34.1	33.8	33.4	33.2	32.7	32.5	31.8	31.5	31.5	31.3
			Score	955	374.5	372.5	370.5	368.5	334	332	329.5	326	323.5	318.5	317	310.5	307.5	307.5	305
		Result	No.	Н	71	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16

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	Q8RXH7 Q8SSE4 Q8VYU0 Q8RYG9 Q8H1Y4 Q9H1X4
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2000 2000 2000 2000 2000 2000 2000 200	251 250 247 246.5 246.5 245.5
11100000000000000000000000000000000000	4 4 4 4 4 4 0 11 12 12 14 15

### ALIGNMENTS

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REPUBLINE=92338377; PubMed=1633311;

RE ROBETES L.M., Tregear J.W., Lord J.M.;

RR ROBETES L.M., Tregear J.W., Lord J.M.;

RR TAGETES L.M., Tregear J.W., Lord J.M.;

RT TATGETED Diagn. Ther. 7:81-97(1992).

-!-CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.

-!-SIMILARITY: BELONGS TRNA.

CC -!-SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR HSSP; P02879; 1BRC

INTERPRO; IPR001574; RIP.

DR HSSP; P02879; IRF001574; RIP.

DR RIPSPO; IPR001574; RIP.

DR RIPSPO; IPR00160; Somatchropin.

Pfam; PF00161; RIP; I.

DR PRINTS; PR00365; SHIGARICIN.

SMART; SM00458; RICIN, 2.

DR ROSITE; PS00231; RICIN, 1.

DR PROSITE; PS00231; RICIN, 2.

PROSITE; PS00238; SOMATGTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                        1 1 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;
                                                                                                          041174;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAN-2003 (TrEMBLrel. 23, Last annotation update)
Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                            PRT;
                                                                        PRELIMINARY;
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                                                                                                                                                               117 LEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQYIE 176
                                                                                                  ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA
                                                  2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 38.4%; Score 374.5; DB 10; Length 580;
l Similarity 48.1%; Pred. No. 3.9e-27;
90; Conservative 26; Mismatches 56; Indels 15; Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE ZES TRINK.
EMBL, AVO39803, AAK82460.1;
-InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; Ricin_B_lectin.
Pfam: PF001627; Ricin_B_lectin, 6.
Pfam: PF00161; RIP; B_lectin, 6.
PRINTS, PR00396; SHIGARICIN.
SWART; SM00458; RICIN; 2.
Hydrolase; Signal; HCLIN, 2.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantary. Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                           10;
                                                                                                                                                                                                                                                                                                                                                   Type 2 ribosome-inactivating protein cinnamomin III precursor (EC 3.2.2.22) (rRNA N-glycosidase).
97.9%; Score 955; DB 10; Length 541; 95.0%; Pred. No. 1.3e-82; ive 0; Mismatches 0; Indels 1
                         0; Indels
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580 AA; 64421 MW; 940D10F01E7FB558 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                           580 AA.
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(TrEMBLrel. 19, Last seg
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                    172 FQYIEGEMRTRIRYNRRSA 190
                                                                                                                                                                                                                        181 FOYIEGEMRTRIRYNRRSA 199
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             Best Local Similarity 95.0
Matches 189; Conservative
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Best Local Similarity
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                                                                                                  52
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  Query Match
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Matches
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Q94BW3
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57 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039802; AAK82459.1; -.
InterPro; IPRO00772; Ricin_B_lectin.
InterPro; IPRO001574; RIP.
Figm.; PF00652; Ricin_B_lectin; 6.
Pfam; PF00651; RIP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang Q., Gong Z.Z., Liu W.Y., "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSN-H
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Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
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TYPE 2 RIBOSOME-INACTIVATING PROTEIN
CINNAMOMIN 11.
3 3784289ECCEOCEPF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.2%; Score 372.5; DB 10; Length 580; 47.6%; Pred. No. 6.1e-27; atlive 27; Mismatches 56; Indels 15;
                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-liactivating protein cinnamomin I precursor
(EC 3.2.2.22) (TRNA N-glycosidase).
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                              Cinnamomum camphora (Camphor tree)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 AA; 64265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gong Z.Z., Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                        PRELIMINARY;
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                                                     208 YRVRESI 214
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177 GEMRIRI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=13429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSN-H 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 92
                                                                                                                                   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purification, characterization and mutageneeis of the A-Chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!-CATALYITC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
BEMBL; AF259548; AAF68978.2; -.
HSSP; P02879; 2AAI.
                                                                             Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
Dilycosidase) (Fragment).
Bukaryota: Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Sperintophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                   38.0%; Score 370.5; DB 10; Length 581;
48.1%; Pred. No. 9.5e-27;
ive 25; Mismatches 57; Indels 15; Gaps
                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039801; AAK82458.1; -.
Cinnamomum camphora (Camphor tree).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                            TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xie L., Liu W.-Y., Wang E.-D.; "Molecular cloning of cinnamomin A-, B-chain and the expression."
                                                                                                                                                                                                                                                                                                                                                           6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                     InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 5.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                            PRINTS; PRO0396; SHIGARICIN.
SMART; SMOG458; RICIN; 2.
PROSITE; PSS0231; RICIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                           581 AA; 64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 GEMRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 YRVRGSI 214
                                                                 SEQUENCE FROM N.A.
Yang Q., Gong Z.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                        NCBI TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=13429
                                                                                                                         patterns.";
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60 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSPVTLAVDVTNAXVVAXRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 LEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                      7 YPIINFTTAGATVQSYTNFIRAVRGRÜT------VLPNRVGLPINQRFILVELSN-H 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTICA ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RANA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AR5367252, PAKS2960.1; -.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae; Trichosanthes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Gaps
                                                                                                                                                                                                                                                                                     DB 10; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%; Score 334; DB 10; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Indels
                                                                                                                                                                                                                                                                                37.8%; Score 368.5; DB 10; Length 48.1%; Pred. No. 1.4e-26; Live 25; Mismatches 57; Indels
                                                                                                                                                                                                                            549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 270 TRICHOSANTHIN.
289 AA; 31706 MW; A6D5602549CA5657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                   PROSITE; PS50231; RICIN_B_LECTIN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
                     InterPro; IPR001574; RIP. — Pfam; PF00652; Ricin B lectin; Pfam; PF00161; RIP; 1.
                                                                                               PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                           1 Similarity 48.13
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 GEMRTRI 183
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                                                                                                                                                                                 Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                        82 IISVAIDVTNVYIMGYRAGDISYFF---NEASATEAAKYVFKDSMRKITLPYSGNYERLO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 INFTTAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng H., Wang B., Shaw P., Yeung H.;
"[Cloning and DNA sequencing of the gene encoding trichosanthin].";
I Chuan Hsueh Pao 21-42-51(1912)
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 288 RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL: $701.76; AAB31048.1; -.
HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Score 332; DB 10; Length 289; 38.9%; Pred. No. 1.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNR
N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (BC 3.2.2.22) (TRNA N-glycosidase)
TRICHOSANTHIN, TCS.
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 A.A.
                                                                                                                                                                                                                                                                                                                     289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
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                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94271613; PubMed=8003348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 38.9:
les 72; Conservative
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                          : |:
194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 MRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 IGKRV 198
                                                                                                                                              179 MRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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004367
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Q41216
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DNLETAAGTRRESIELGPSPLDGAITSLYYDE-----SVARSLLVVIQMVSEAARFRY 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YPIINFTTAGATVOSYTNFIRAVR-----GRLTVLPNRVGLPINORFILVELSNH 56
                                                                                                                                                                                                                                                                                          "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; Plant 5. 12:1251-1260(1997).
-!- CATALYIC ACTIVITY: ENDOWTDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trichosanthes sp. Bac Kan 8-98.
Bukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 RIBOSOME INACTIVATING PROTEIN, A CHAIN.
563 RIBOSOME INACTIVATING PROTEIN, B CHAIN.
62336 MW; 3ED2B6C08E796205 CRC64;
                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 563;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last amnotation update)
Trichobakin (EC 3.2.2.22) (TRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                     Jan Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 329.5; DB 1 40.5%; Pred. No. 7.5e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U76524, AAC15886.1, --
HSSP, P02079, 2AAI.
InterPro, IPR000772, Ricin_B_lectin.
InterPro, IPR001574, RIP.
Pfam, PF00652, Ricin_B_lectin, 6.
Pfam, PF00161, RIP, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Signal; Toxin.
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                                                                                                                                                                                                         MEDLINE=98112023; PubMed=9450339;
Sambucus nigra (European elder)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
wes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids I; Cucurbi
NCBI_TaxID=118182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=4202;
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298
                                                                                                                                                                                                                                                                    Peumans W.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                         122 GNLRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFITAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                61
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AB039324; BAA92530.1; -.
HSSP; P09989; 1NRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENCOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AJ400822; CAC33178.1; --
                                                                                                                                                                                                                                                                                                                33.4%; Score 326; DB 10; Length 247;
39.6%; Pred. No. 5.2e-23;
Live 44; Mismatches 50; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, campamulids; Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L., "Molecular cloning of ebulin 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA
N-glycosidase).
                                                                                                                                                                                247 247
247 AA; 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 AA
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SMART; SM00458; RICIN; 2.
PROSITE; PS00271; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN, 1.
Glycosidase; Hydrolase; Signal; Toxin.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                               PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                             InterPro; IPR001574; RIP. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                            72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02879; 2AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                Hydrolase, Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sambucus ebulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 RI 183
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                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                   7 YPIINFTTAGATVQSYTNFIRAVRGR-----LITVLPNRVGLPINQRFILVELSNH 56
                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ODQVIKFTTEGATSOSYKOFIEALKORLIGGLIHDIPVLPDPTTVEERNRYITVELSNSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by CDNA
sequencing: conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
-!-CATALYTY CATIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!-SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
BKNB1, M98346, AAA32626.1;
-InterPro; IPRO00772; Ricin B.lectin.
InterPro; IPRO01572; Ricin B.lectin.
Pfam; PF00652; Ricin B.lectin; 6.
                                                                                                                                57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last anotation update)
01-NAR-2003 (TrEMBLrel. 23, Last anotation update)
Abrin-d (EC 3.2.2.2) (rRAM N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                        25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
                               Query Match 33.2%; Score 323.5; DB 10; Length 564; Best Local Similarity 40.0%; Pred. No. 2.8e-22; Matches 76; Conservative 38; Mismatches 51; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Indels
62694 MW; 8261681A6DB55CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.7%; Score 318.5; DB 10
43.3%; Pred. No. 7.7e-22;
tive 22; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PR00396; SHIGARICIN.
SMART, SMORES, RICIN, 2.
PROSITE, PS5021; RICIN B LECTIN, 2.
PROSITE; PS00275; SHIGA RICIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   195 İEQEVRRSLO 204
                                                                                                                                                                                                                                                                                                                       175 IEGEMRTRIR 184
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564 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3816;
SEQUENCE
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             63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
"Trichosathes Airilowii trichosathin precursor (TCS) gene.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                              Trichosanthes Kirilowii (Mongolian snake-gourd).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY082348; AAM22782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.5%; Score 317; DB 10; Length 270; 36.8%; Pred. No. 4.3e-22;
                                                                                                                                                                      54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
29683 MW; 531713B754F9B769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
(EC 3.2.2.22) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 AA.
                                                                                                                                              270 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRICHOSANTHIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anna
Abrin-E (RRNA N-glycosidase) (EC 3.2.
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Conservative
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 >270
                                                   178 EMRTRIR 184
                                                                            174 RVGVSIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 2
270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           Fragment).
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SEQUENCE
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                                                                                                                                             Q8LPV7
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                                                                                                                  RESULT 12
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66 EVGIDVTNAXVVAXRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 HQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRVGV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRECEDES ENDOCYTOSIS.

-! CATALYTIC ANDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, BESCH DOMAIN
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROPERSY: CARABEGA1; -- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING REMBL: X54872; CARABEGA1; -- RIP.
HSSP: PI1140; LABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFITAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 IXFSTEGATSQSYKOFIEALRERLRGGLIHDIPVLRDPTTVEERNRYITVELSNSERESI
                  Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sambucus nigra (European elder).
Sukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                            J. Biol. Chem. 266:6848-6852(1991).

-i- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADBINE FROM POSITION 4,324 OF 28 S RNNA-ARRIN-A IS MORE TOXIC THAN RICIN.

-i- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                  Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.8%; Score 310.5; DB 10; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00161; Kif, 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PR00275; SHIGA RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; A CHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein (EC 3.2.2.22) (rRNA N-glycosidase).
precatorius (Indian licorice) (Crab's eye)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.2%; Pred. No. 1.6e :ive 22; Mismatches
                                                                                                                                                                             MEDLINE=91201329; PubMed=2016300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001574; RIP.
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                                                                                                                                SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 RIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 SIR 181
                                                                                                                                                        TISSUE=LEAF
                                                                                                                                                                                                                                            chains.";
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NCBI\_TaxID=4202;

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57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFIDVQNRYIFAFGGNY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVR------GRLTVLPNRVGLPINQRFILVELSNH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87
                                                                                           "Characterization and cloning of lectins and ribosome-inactivating proteins from Sambucus nigra leaves."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYZIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Girbes T., Arias F.J., Antolin P.;
"Characterization and molecular cloning of Nigrin 1, a type two
"Characterization and molecular cloning of Nigrin 1, a type two
ribosome.inactivating protein from leaves of elder (Sambucus nigra).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF249280; AAN86130.1;
Hydrolase; Glycosidase.
SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Gaps
                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF409135; AAL04123.1; -.
INTERPRO; PROMOTY2; Ricin B lectin.
InterPro; IPR001574; Ricin B lectin.
Pfam; PP00652; Ricin B lectin; 6.
Pfam; PP00652; Ricin B lectin; 6.
PROMITS; PR00396; BHIGARICIN.
PROSITE; PS50231; RICIN; B LECTIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1 ype 2 ribosome-inactivating protein nigrin 1 precursor
(EC 3.2.2.2)
Sambucus nigra (European elder)
Sambucus nigra (European elder)
Spermatophyta; Vizidiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         31.5%; Score 307.5; DB 10; Length 563; 38.4%; Pred. No. 9.5e-21; Live 36; Mismatches 56; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Toxin. -
SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 38.4
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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195 IEQEVRRSLQ 204
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                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Leaf;
                                                                           Van Damme E.J.M.;
                                                         rissum=reaf;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

25;

Query Match
Best Local Similarity 38.4%; Pred. No. 9.5e-21;
Matches 73; Conservative 36; Mismatches 56; Indels 25;

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88 NGNITVILAVDVINLYVVAFSGNANSYFF----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
                                                                                                                                                               57 AELSVIIALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 114
                                                                                                                                           115 DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTOMISEAARFQY 174
-----GRLTVLPNRVGLPINQRFILVELSNH 56
                        Search completed: February 10, 2004, 16:26:40 Job time : 26.3521 secs
7 YPIINFTTAGATVQSYTNFIRAVR--
                                                                                                                                                                                                                                     || |:| ::
195 IEQEVRRSLQ 204
                                                                                                                                                                                                                  175 IEGEMRTRIR 184
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